GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

	- nucleic search, using sw model May 18, 2004, 16:14:01 ; Search tim	(Without alignments) 8816.891 Million cell updates/sec	. US-10-681-972-12 ore: 286 I gggaattcggatccaagaaataataaggatccgaattccc 286	ble: IDENTITY NUC Gapop 10.0 , Gapext 1.0	3470272 segs, 21671516995 residues	er of hits satisfying chosen parameters: 6940544	seq length: 0 seq length: 200000000	ssing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	GenEmbl:*  1: gb ba:*  1: gb ba:*  3: gp_in:*  5: gb ov:*  6: gb pat:*  6: gb pat:*  10: gb pr:*  10: gb pr:*  11: gb r:*  11: gb r:*  11: gb r:*  12: gb v:*  13: gb v:*  11: gb r:*  12: gb v:*  13: gb v:*  13: gb vi:*  14: gb vi:*  15: gb vi:*  16: em_fun:*  17: em_hum:*  18: em_fun:*  18: em_fun:*  20: em_ov:*  21: em_ov:*  22: em_pi:*  22: em_lin:*  23: em_lin:*  24: em_lin:*  25: em_lin:*  26: em_vi:*  27: em_lin:*  28: em_lin:*  29: em_lin:*  29: em_lin:*  20: em_lin:*  30: em_lin:*  40: em_lin:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AR014689 Sequence AR432389 Sequence	AR014691 Sequence	AR432391 Sequence	ARVI4086 Sequence AR432386 Sequence	AR014682 Sequence	Ak432382 Sequence U59459 Brassica na	X97319 R. sativus m	E31545 Antibacteri AB012871 Wasabia i	U18557 Raphanus sa	A26875 R.sativus A A39549 Semience 37	A63404 Sequence 19	ARUSUISS Sequence AR130272 Sequence	123728 Sequence 48	AR374914 Sequence	AF528180 Brassica E31546 Antibacteri	BD174927 Disease t	AY383485 Brassica A68645 Sequence 13	X91916 A.thaliana	AIVSZZS6 AIGDIUOPS A68647 Sequence 15	AY063779 Arabidops	A39553 Sequence 41	AR050161 Sequence	Akisozeo Sequence 123736 Sequence 58	AX412329 Sequence	AX412502 Sequence AX507351 Sequence	AX590057 Sequence	AIL33/8/ Arabidops AR014692 Sequence	AR432392 Sequence	AX412601 Sequence	AX651878 Sequence	co.		DNA linear PAT 05-DEC-1998 5.			Shun. and Rosenberger, C.Annette. s for controlling plant pathogenic	
SUMMARIES	ID	AR014689 AR432389	AR014691	AR432391	AR432386	AR014682	AK432382 BNU59459	RSEFP3	E31545 AB012871	RSU18557	A26875 A39549	A63404	AR130272	I23728	AR374914	AF528180 E31546	BD174927	AY383485 A68645	ATANTSPEC	A1052236 A68647	AY063779	A39553	AR050161	AK130280 123736	AX412329	AX412502 AX507351	AX590057	A1133/8/ AR014692	AR432392	AX412601	AX651878	ALIGNMENTS		286 DP ent US 5773696	<b>4.</b> 3.		anlal., Wu,Y.Shun de and methods fo	12 30-JUN-1998
	Length DB	286 6 286 6																																2 from pat	GL:39/2L	ed.	1 to 286) Shah, D.Maganlal polypeptide an	5773696-A
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Unclassified.
1 (Dases 1 to 270)
Liang, J., Shah, D.Maganlal., Wu, Y.Shun. and Rosenberger, C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
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Lichases 1 to 270)

Liang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.

Antifungal polypeptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi
Patent: US 6652280-A 14 25-NOV-2003;

Location/Qualifiers
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AR432391.1 GI:40194668
                                                                                                                                                                                                                                                                                                                                                    /mol_type="unassigned DNA"
                                                                                                270 bp
US 5773696.
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Sequence 14 from patent
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1 (bases 1 to 286)
Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
Antifungal polypeptide AlyAFP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 12 25-NOV-2003;
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100.0%; Score 286; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.9e-71;
Matches 286; Conservative 0; Mismatches 0;
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Sequence 12 from patent US 6653280.
AR432389
                                                   /mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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                                  /organism="unknown"
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Pred. No. 4.9e-44;
0; Mismatches 33;
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1 (bases 1 to 308)
Liang, J., Shah, D.Maganlal., Wu, Y.Shun.
Antifungal polypeptide and methods for
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/mol_type="unassigned DNA"
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Location/Qualifiers
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Sequence 5 from patent US 5773696.
AR014682. GI:3972136
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                 GI:40194663
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Best Local Similarity 86.1%;
Matches 223; Conservative (
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AR432386.1
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AR014682
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.
Unclassified.
1 (bases 1 to 500)
Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
                                                                                                                                                                                                                                                                                                                                                      PAT 05-DEC-1998
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                                                                                  GCTCTTGTTCTCTTTGCTGCCTTTGAAGCACCACAACAATGGTGGATGCAAGGTTGTGCGAG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 ATCACAGAAAGTAATAGATATGGCTAAGTGTGCTTCCATCATCTCCCTTGTCTCTGCTGC 109
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                                                                                                     GCTCTTGTTCTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGAAGGTTGTGCGAG
                                                                                                                                         188 CAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAATG
                                          AGAAACCTTGAAAGAGGGAACACGGATCTTGCAACTATGTCTTCCCCAGCTCACAAATGT
                                                                                                                                                                                                                          181 AGAAACCTTGAAAGAGCAGAACACGGATCTTGCGAACTATGTCTTCCCAGCTCACAAATGT
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Pred. No. 1.8e-51;
0; Mismatches 19; Indels
                            GGATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTC
  Indels
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                                                                                                                                                                                                                                                                      241 ATTGTTACTTCCCATGTTAATAAGGATCC 270
                                                                                                                                                                                                                                                     249 ATTIGITACTICCCAIGITAATAAGGAICC 278
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
/wol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent: US 5773696-A 9 30-JUN-1998;
Location/Qualifiers
1. .500
                                                                                                                                                                                                                                                                                                                                                    AR014686 500 bp
Sequence 9 from patent US 5773696.
AR014686.1 GI:3972140
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Sequence 9 from patent US 6653280.
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  5;
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Best Local Similarity 91.6%;
Matches 241; Conservative
 268; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown.
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AR432386
LOCUS
DEFINITION
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TITLE
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AR014686
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/codon_start=1
/product="antifungal protein"
/protein_id="AAB03224.1"
/db_xref="GI:139230"
/translation="WAKFASIITLLFAALVVFAAFEAPTMVBAKLCERSSGTWSGVCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLN 31-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Raphanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGGATCATGCAACTATGTGTTCCCTGCTCACAAGTGTATCTGTTATTTCCCATGTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 CACGGAICTIGCAACTAIGTCTICCCAGCICACAAAIGTATTIGITACTICCCAIGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGCTAAGTTTGCTACCATCATCTCTTTCTCTTTGCTGCTCTTGTTCTCTTTTGCTGCC
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                                                                                                                                                                                                                                                                            /db xref="taxon:3708"
/note="transcript putatively induced by Screrotinia
screrotium in infected Brassica napus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Terras,F.R.G., Goderis,I.J., Penninckx,I.J., Osborn,R.W. and
Broekaert,W.F.
Unpublished
                                                                               Sohn, U., Lee, C.M., Lee, M.H. and Kim, J.H.
Direct Submission
Submitted (129-MAY-1996) Department of Genetic Engineering,
Kyungpook National University, Puk-Ku, Sankyuk-Dong 1370,
702-701, Korea
On Jul 1, 1996 this sequence version replaced gi:1293377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Indels
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Terras, F.R.G.
Direct Submission
Submitted (09-AFR-1996) F.R.G. Terras, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.2%; Score 186.6; DB 8;
larity 85.9%; Pred. No. 7.8e-43;
Conservative 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  475 bp mRNA
R.sativus mRNA for antifungal protein 3.
X97319
1 (bases 1 to 451)
Sohn, U., Lee, C.M., Lee, M.H. and Kim, J.H.
Brassica napus cDNAs
                                                                                                                                                                                                                             /organism="Brassica napus"
                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="Naehan"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X97319.1 GI:1655684
AFP; antifungal protein 3.
Raphanus sativus (radish)
Raphanus sativus
                                                                      (bases 1 to 451)
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                                              Unpublished
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207; Conserv
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Best Local S
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KEYWORDS
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AUTHORS
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Brassica napus
Brassica napus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae,
                                                                    229
                                                                                                                      169
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                                                                                                  188 CAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCCAGCTCACAAATG 247
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                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.

1 (bases 1 to 308)

1 (lang, U., Shah, D.M., Wu, Y.S., and Rosenberger, C.A.
Antifungal polypeptide AlyAFP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 5 25-NOV-2003;

Location/Qualifiers
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US9459 H07366
US9459.1 GI:1399229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 66.7%; Score 190.8; DB 6; Length Best Local Similarity 86.1%; Pred. No. 4.9e-44; Matches 223; Conservative 0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                      308 bp
308 cgquence 5 from patent US 6653280.
AR432382.1 GI:40194659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .308
/organism="unknown"
                                                                                                                                                                       248 TATTTGTTACTTCCCATGT 266
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VERSION
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AR432382
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TITLE
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209 205

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AB012871
Wasabia japonica mRNA for gamma-thionin1, complete cds.
AB012871
AB012871. GI:11691893
gamma-thionin1.
Butrema wasabi
Eutrema wasabi
                                                    MASAHIRO NISHIBARA, SABURO YAMAMURA
CIZNIS/09, A01HS/00, A01N63/00, C07K14/415, C12N5/10, C12P21/02//
(C12N15/09, C12R1:91), (C12N5/10, C12R1:91), (C12P21/02, C12R1:91),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Eutrema.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-APR-1998) Masahiro Nishihara, Iwate Biotechnology Research Center, Genetic Engineering; 22-174-4 Narita, Kitakami, Iwate 024-0003, Japan (E-mail:mnishiha@sv02.ibrc.pref.iwate.jp, Tel:81-197-68-2911, Fax:81-197-68-3881)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 GAACACGGATCTIGCAACTATGICTICCCAGCICACAAAIGIAITIGITACTICCCAIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CGACATGGATCTTGCAACTATATCTTCCCATATCACAGATGTATCTGTTACTTCCCATGT
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1 (sites) ---- Saitch, H., Kiba, A., Nishihara, M., Yamamura, S., Suzuki, K. Terauchi, R.
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                                                                                                                                                                                                                                                                                                                                Length 414;
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                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                         Query Match 62.9%; Score 179.8; DB 6; Best Local Similarity 84.3%; Pred. No. 7.2e-41; Matches 215; Conservative 0; Mismatches 37;

    .414
    /organism="Eutrema wasabi"
/mol_type="genomic DNA"
    /db_xref="taxon:75806"

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Nishihara,M. and Yamamura,S.
Direct Submission
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                                                                                                                                                                                                                                                                                                      /db_xref="GOA:024332"
| db_xref="SWISS-PROT:024332"
| translation="WAKRASIVALLEAALVVFAAFEAPTVVEAKLCERSSGTWSGVCG
NNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II; Brassicales, Brassicaceae; Eutrema.
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 und Entwicklungsbiologie, Weinberg 3,
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                                                                                     /mol_type="mRNA"
/cultivar="Ronde Rode Kleine Witpunt"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 186.2; DB 8;
Pred. No. 1e-42;
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Patent: JP 19993113678-A 1 16-NOV-1999;
                                                                                                                                                                                                                                     'codon_start=1
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db_xref="GI:1655685"
                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="AFP"
/product="antifungal protein 3"
                                                                    organism="Raphanus sativus"
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Pflanzenbiochemie, Stress- ur
Halle (Saale), D-06120, FRG
Location/Qualifiers
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Masahiro, N. and Saburo, Y.
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JP 1999313678-A/1
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83.1%;
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/gene="AFP"
.115. .264
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                                                                                                                                                                                    'gene="AFP"
28. .267
                                                                                                                                                                                                                   'gene="AFP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212; Conservative
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Best Local S:
Matches 212
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/Godon_start=1
/evidence=experimental
/evidence=antifungal protein 1 preprotein"
/protecin id="AAA69541.1"
/db_xref="G1:609322"
/translation="WAKFASITALLPAALVLFVAAFEAPTMVEAQKLCERPSGTWSGVCGNNACKNQCINLEKARHGSCNYVFPAHKCICYFPC"
                                                                                                                                                                                                                                                                                                                                                  /product="antifungal protein 1"
/function="antifungal, fungistatic"
/function="antifungal, fungistatic"
/note="Evidence for antifungal activity: Analysis of two novel classes of antifungal proteins from radish (Raphanus sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
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BIOCLIDAL PROTEINS
Patent: WO 9305153-A 33 18-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 8; Length 395;
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                                                                                                                  function="antifungal, fungistatic"
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Chem. 267, 15301-15309"
/citation=[1]
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        'db_xref="taxon:3726"
                        'tisue_type="seed"
|. .395
|gene="Rs-AFP1"
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                                                                                                                                                                                                                                                                                                 gene="Rs-AFP1"
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/gene="Rs-AFP1"
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A26875
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                                                                                         /codoi_start=1
/podoit= gamma-thionin1"
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/db_xref="G1:11691894"
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GNNNACKNQCINLEGARHGSCNYIFPYHRCICYFPC"
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Raphanus sativus antifungal protein 1 preprotein (Rs-AFP1) mRNA,
complete cds.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Raphanus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
of Genetics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-3001
On Feb 9, 1995 this sequence version replaced gi:609321.
                                                                                                                                                                                                                                                                                                                                                                                             83
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/strain="ronde rode kleine witpunt"
                                                         'tigsue_type="leaf and stem"
....243
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'mol_type="mRNA"
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88. .240
/product="unnamed"
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AUTHORS
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JOURNAL

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COMMENT FEATURES

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186 TGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTA 245
                                                                                                                            Search completed: May 18, 2004, 17:59:03
Job time : 1407.95 secs
                                               257 CTTCCCATGTTAAT 270
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unidentified
unclassified.

ACE 1 (bases 1 to 414)

ORS Dubock, A.C., Powell, K.A. and Rees, S.B.

ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS

ANTIMICROBIAL-PROTEIN-1994;

ZENECA LITD (GB)

ZENECA LITD (GB)

Cocation/Qualifiers

Location/Qualifiers

AA4

"...identified"
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Pred. No. 1.4e-40;
0; Mismatches 37; Indels
                                                                                                                         Query Match 62.5%; Score 178.8; DB 6; Length Best Local Similarity 84.3%; Pred. No. 1.4e-40; Matches 214; Conservative 0; Mismatches 37; Indels
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                             1. .414
/organism="Raphanus sativus"
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Sequence 37 from Patent W09416076.
A39549.1 GI:2295842
              Location/Qualifiers
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Best Local Similarity 84.3%;
Matches 214; Conservative (
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

May 18, 2004, 16:12:26 ; Search time 278.85 Seconds (without alignments) 4357.126 Million cell updates/sec

US-10-681-972-12 Title: Perfect score:

1 gggaattcggatccaagaaa......taataaggatccgaattccc 286 Sequence:

IDENTITY\_NUC Gapopt 10.0 Scoring table:

3373863 segs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

N Geneseq 29Jan04:\* Database :

geneseqn1980s:\*
geneseqn2000s:\*
geneseqn2001as:\*
geneseqn2001as:\*
geneseqn2002s:\*
geneseqn2003as:\*
geneseqn2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:\*

## SUMMARIES

SUMMAKIES	Description	1574 Aat94574 Alvssum s	Aat94582		1 Aat94581	7 Aat94577	3 Aaz39123	Aaq38650	Aaq70128	e	Aat68696	Aaz39124	Abq82690	Aav10632	Aav10633 A.	Abq82691 Was	Aaq38652	)130 Aaq70130 Antimicro		136 Arabidops	1 Adc51221	3378 Arabidops	3 Adc51223	
ă	QH QH	AAT9457	AAT94582	AAT99289	AAT9458	AAT9457	AAZ3912	AAQ38650	AAQ70128	AAT7233	AAT68696	AAZ39124	ABQ82690	AAV10632	AAV10633	ABQ82691	AAQ38652	AAQ7013	ABZ14241	ABZ42136	ADC5122	ADA68378	ADC5122	
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e¥.	Query Match	100.0	94.1	89.8	75.7	66.7	62.9	62.5	62.5	62.5	62.5	62.3	62.0	61.7	61.6	61.5	61.2	61.2	6.09	60.9	60.3	59.8	59.2	
	Score	286	269.2	256.8	216.6	190.8	179.8	178.8	178.8	178.8	178.8	178.2	177.4	176.6	176.2	175.8	175	175	174.2	174.2	172.6	171	169.4	
	Result No.		7	m	4	S	9	7	ထ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	

This sequence encodes the mature protein of an antifungal polypeptide (AlyARP) isolated from plants of the genus Alyssum. The sequence was PCR amplified using primers AAT94583-194584, and the resultant 264 bp fragment was cloned as a BamHI fragment into the expression vector pMONI23317 to generate plasmid pMONI2552. The AlyARP sequence in this

Claim 12; Page 68; 92pp; English.

24 166 58.0 449 3 AAA53190 25 155 54.2 1973 3 AAC46924 26 120.8 42.2 1616 2 AAV10646 27 116.2 4 0.6 5 606 3 AAZ99326 28 115.4 40.3 552 3 AAZ99326 31 115.4 40.3 534 3 AAZ99327 31 115.4 40.3 534 3 AAZ99327 31 115.4 40.3 534 3 AAZ99337 111.6 39.0 437 3 AAZ9933 111.6 39.0 437 3 AAZ9933 37 107.4 37.6 485 3 AAZ9933 41 107.4 37.6 486 3 AAZ99336 42 107.4 37.6 486 3 AAZ99336 42 107.4 37.6 486 3 AAZ99336 43 107.4 37.6 557 3 AAZ99336 44 76.8 26.9 284 2 AAQ38651 45 76.8 26.9 284 2 AAQ38651	Aaa53190 Raphanus	Aac46924 Arabidops	Aav10646 A. thalia		Aaz99324 DNA encod	-	_	DNA	_	Clor	_	DNA	7 DNA	DNA	DNA	DNA	DNA	DNA			Trun	5	
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	24	25	26	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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/product= "mature AlyAFP protein"
/note= "no start codon given at 5' end of sequence"
                                                                                                                                                                                                                                                                                                                                         Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi.
                                                                                          Antifungal polypeptide; AlyAFP; inhibition; transgenic plant; phytopathogenic fungus; resistance; ss.
                                                                       Alyssum species anti-fungal polypeptide AlyAFP cDNA sequence.
                                                                                                                                                                                                                                                                                            Rosenberger CA;
                                                                                                                                         Location/Qualifiers
                   BP.
                 AAT94574 standard; cDNA; 286
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                                                     12-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                         Shah D, Wu Y,
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P-PSDB; AAW35558.
                                                                                                                                                                                                                                                                         (MONS ) MONSANTO CO.
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                                                                                                                       Alyssum sp.
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RESULT 1
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plasmid is placed under control of an E35S promoter and the maize HSP70 intron I sequence. The protein can be used to control phytopathogenic fungi, whilst the DNA can be used to produce transgenic plants that express the protein making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                     GGGAATTCGGATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTTC
                                                                                                                                                                                                                                                               TCTTTGCTGCTCTTGTTCTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCAAGGT
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                                                                                                                                                          Gaps
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                                                                                                                        Length 286;
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                                                                                                                                                         Indels
                                                                                     Sequence 286 BP; 80 A; 62 C; 65 G; 79 T; 0 U; 0 Other;
                                                                                                                    100.0%; Score 286; DB 2;
100.0%; Pred. No. 4.8e-81;
ive 0; Mismatches 0;
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109. .258
/*tag= c
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                                                                                                               Ouery Match
Best Local Similarity 100.
Matches 286; Conservative
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P-PSDB; AAW35560.
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                                This sequence represents the cDNA sequence cloned into the E. coli cassette vector pMON23317 to generate vector pMON22652. The cDNA encodes the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum. The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic
                                                                                                                                                                                                                                                                                                                                                        AGAAACCTIGAAAGAGCAGAACACGGAICTIGCAACTAIGTCTICCCAGCICACAAIGT 248
                                                                                                                                                                                                                                                                                GCTCTTGTTCTCTTTGCTGCCTTTGAAGCAACAATGATGGTGGATGCAAGGTTGTGCGAG 120
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                                                                                                                                                                                                                                                                                                                                AGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGT 240
                                                                                                                                                                                                                                                         GCTCTTGTTCTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCAAGGTTGTGCGAG 128
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                                                                                                                                                                                                                                                                                                          GGATCCAASAAAGTAATAGWTATGGCTAAGTTTGCTACCATCATCTCTTCTTCTTTGCT
                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antifungal polypeptide, AlyAFP; inhibition; transgenic plant; phytopathogenic fungus; resistance; ss.
                                                                                                                                                        Score 269.2; DB 2; Length 270; Pred. No. 1.1e-75; 2; Mismatches 0; Indels 0
                                                                                                                                                                                                          GGATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "AlyAFP antifungal polypeptide"
                                                                                                                                 Sequence 270 BP; 75 A; 58 C; 60 G; 75 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                      ATTIGITACTICCCARGITAATAAGGAICC 270
                                                                                                                                                                                                                                                                                                                                                                                                        ATTIGITACTICCCATGITAATAAGGATCC 278
                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alyssum species AlyAFP cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
           Example 4; Page 69; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР
                                                                                                                                                       94.1%;
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439. .443
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                                                                                                                                                                     Best Local Similarity 99.3 Matches 268; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT99289 standard; DNA;
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                                                                                                                                                                   Similarity
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                                                                                                                                                         Query Match
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This sequence represents the cDNA sequence encoding the antifungal polypeptide AlyAFP, from plants of the genus Alyssum. The sequence represents a composite of the sequences isolated by 5' and 3' RACB (Rapid Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 CAGAAACCTIGAAAGAGCAGAACACGGATCTIGCAACTAIGTCTICCCAGCTCACAAAIG
                                                                                                                                                                                                                                                                                                   50 ATCACAGAAAGTAATAGATATGGCTAAGTGTGCTTCCATCATCTCCCTTGTCTGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                               170 GAGICCAAGIGGAACAIGGICAGGCGIGIGIGGGAAIAAIAACGCAIGCAGGAACCAAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCCAGCTCACAAATG
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Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi
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                                                                                                                                                                                                                     DB 2; Length 500;
                                                                                                                                                                                         Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                   75.7%; Score 216.6; DB 2; ilarity 91.6%; Pred. No. 9.2e-59; Conservative 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloned 5' region of antifungal polypeptide cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA;
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                                            Example 4; Page 67; 92pp; English.
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                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                        This sequence represents the cDNA sequence which encodes the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum. The AlyAFP polypeptide can be used to control phytopathogenic fungii, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                     190
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                                                                                                                                                                                                                                                                                                                                                      TCTTGTTCTCTTTGCTGCCTTTTGAAGCACCAATGGTGGATGCAAGGTTGTGCGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCCAGCTCACAAATGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composite cDNA sequence for Alyssum species antifungal polypeptide.
                                                                                  Alyssum antifungal polypeptide and corresponding DNA - used in the
                                                                                                 production of transgenic plants resistant to phytopathogenic fungi
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                                                                                                                                                                                                                                                                            Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antifungal polypeptide; AlyAFP; inhibition; transgenic plant. phytopathogenic fungus; resistance; ss.
                                                                                                                                                                                                                                                                          Score 256.8; DB 2; Length
Pred. No. 1.3e-71;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                               Sequence 481 BP; 147 A; 88 C; 91 G; 154 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                    11 ATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCT
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             Rosenberger CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 TTGTTACTTCCCATGTTAAT 293
                                                                                                                              Example 4; Fig 1; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.2%;
Matches 258; Conservative 0
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             Wu Y,
                                         WPI; 1997-503109/46.
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             Shah D,
                                                        P-PSDB; AAW35560
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             Liang J,
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109 127 169 187 229 247

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This sequence is the product of the amplification of the 5' region of the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum, by a 5' RACE (Rapid Amplification of cDNA Ends) using priners AAT94575-194576). The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                            An antibacterial protein gene of Wasabia japonica - useful as a food- or
                                                                                                                                                                                                                                                                                                               110 rcingircrciringciecriringaagcaccagcaargergeagcacaagricigda
                                                                                                                                                                                                                                                                                                                                                                     170 GAGTCCAAGTGGAACATGGTCAGGCGTGTGTGGAAACAACAACAATGCTTGCAAGAATCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                          CAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATG
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                                                                                                                                                                                                                                                                                    TCTTGTTCTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGA
                                                                                                                                                                                                                                                                                                                                               Wasabia japonica antibacterial protein encoding cDNA SEQ ID NO:1.
                                                                                                                                                             Score 190.8; DB 2; Length 308;
Pred. No. 1.3e-50;
0; Mismatches 33; Indels 3;
                                                                                                                                  78 A; 71 C; 78 G; 79 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wasabia japonica; antibacterial; food additive; ds

    243
    *tag= a
    'product= "antibacterial protein"

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                                                                                                                                                Query Match
Best Local Similarity 86.12
Best Local Similarity 86.12
Conservative
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(first entry)
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                                                                                                                                  Sequence 308 BP;
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01-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTACTTCCCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CGACATGGATCTTGCAACTATGTTTCCCATATCACAGATGTATCTGTTACTTCCCATGT
                                                                                                                                                                                                                                                                                                                                           1 ArgectaActriccircrarcarcecterretrecerecterretretretretre
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                                                                                                                                                                                                                                                                                                                                                                                                90 TITGAAGCACCAACAATGGTGGATGC---AAGGTTGTGCGAGAGACCAAGTGGGACATGG
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                              from
                      The present sequence encodes an antibacterial protein isolated fro
Wasabia japonica. The antibacterial protein can be used as a food
additive. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                           3,
                                                                                                                                                                              Score 179.8; DB 3; Length 414;
Pred. No. 4.8e-47;
0; Mismatches 37; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Terras FRG;
                                                                                                                                                                                                                                                                                          30 AIGGCIAAGTITGCTACCATCATCTCTTCTCTTTGCTGCTCTTGT
                                                                                                                                 Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rees SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osborn RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
16. .256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ38650 standard; DNA; 414 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91GB-00018523.
92GB-00003038.
92GB-00013526.
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                                                                                                                                                                                 62.9%;
Best Local Similarity 84.3%;
Matches 215; Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raphanus sativus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-1991;
13-FEB-1992;
25-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Broekaert WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RS-AFP1 CDNA
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07-JUL-1993
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Powell KA,
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                                         WPI; 1994-249223/30.
                                                                                                                                                                                                                                  correct PN field.)
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                                                       P-PSDB; AAR57325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9721815-A2
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               Dubock AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT72333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage R408. Inserts from 22 positive clones were excised by BcRI digestion and their size compared by agarcase gel electrophoresis. Four clones had insert sizes of approx. 400bp the others between 250-300bp. The inserts of the 4 largest clones were then sequenced and found to differ only in the length of their 5, and 3, VTR's. The longest sequence is given here. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                            80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                      125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 TGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCT 185
                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial; Rs-AFF1; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 ritriscriscriticsaascaccaacaarsarssascacasaastristiscsaaaseccaas
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                                                                                                                                                                                                                                                                                                                                                                                              6 ATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCT
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                            ä;
                                                                                                                                                                                                                                                                                                               Score 178.8; DB 2; Length 414; Pred. No. 1e-46; 0; Mismatches 37; Indels 3.
                                                                                                                                                                                                                                                                                       Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
            Example 21; Fig 35; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                               62.5%;
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                                                                                                                                                                                                                                                                                                                                           Matches 214; Conservative
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                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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14-FEB-1995
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                                                                                                                                                                                                                                                                                                             Plant-derived antimicrobial proteins are expressed in endosymbiotic clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFPI from R. sativus. The full-length CDNA sequence of Rs-AFPI is given in AAQ70128. (Updated on 25-MAR-2003 to
                                                                                                                                  Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 TGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 ATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .87, aa:Glu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raphanus sativus antifungal protein I (Rs-AFP1) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
62.5%; Score 178.8; DB
Best Local Similarity 84.3%; Pred. No. 1e-46;
Matches 214; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (pos:85.
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                                                                                                                                                                                                                                                         Disclosure; Page 31; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/transl_except= (
16. .102
Rees SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT72333 standard; cDNA; 414 BP.
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103. .255
/*tag= c
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ä

96WO-GB003068

12-DEC-1996;

19-JUN-1997

= ÷ Radish antifungal protein 1 (Rs-AFP1) cDNA

related

Sijtsma L, Van Amerongen A; Borremans FAM, Rees SB;

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Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
                                                                         Puijk WC, Schaaper WMM,
, Samblanx GW, Fant F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                           Claim 8; Fig 2; 65pp; English.
                                                                                                                                                                                                                                                                                                          62.5%;
                                    95GB-00025455
96GB-00006552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT68696 standard; cDNA; 414
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Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTCCTTGTTAAT
                                                                                                       WPI; 1997-332786/30.
P-PSDB; AAW19280.
                                                          (ZENE ) ZENECA LID
                                                                         Meloen RH, Pui;
Broekaert W, Sa
Van Gelder WMJ;
                                    13-DEC-1995;
28-MAR-1996;
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                                                                                                                                                                                                                                                                            field.
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                                                                                                                                                                                                                                                                                                                                                                                   임
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136 125 196 185 256 186 richanandehedarchiceneriachacharierereceneerenen 245 79 65 protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct crops, protein (Rs-AFP1). Analogues of the homologous protein, Rs-AFP2
(AAM12281), have also been produced (see AAW19282-92, AAW19294-98,
AAW19301-04, AAW19303-34 and AAW1765-8131. Platus containing DNA
sequences encoding these proteins have improved resistance to fungi.
Compositions containing the peptides can be used to control fungi or
bacteria in pharmaceutical (e.g. treatment of Candida infections) or
preservative purposes (as food additives). In agriculture, the peptide
may be used to improve disease resistance or disease tolerance of crops
either pre or post harvest. When applied to plants they may also have CTITIGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 66 ritriciocitricca accacca acta a recica a caca a caca a constructor a caca a constructor a caca a TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA Gaps This cDNA sequence encodes an Rhapanus sativus (radish) antifungal 3; Length 414; 37; Indels Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other; Score 178.8; DB 2; Pred. No. 1e-46; 0; Mismatches Score 178.8;

This cDNA clone codes for the preprotein for radish antifungal protein 1 (Rs-AFP1) (AAW19617). Novel antifungal proteins are based on Rs-AFP1, Rs-AFP2 (see AAW19616), Rs-AFP3 and Rs-AFP4, especially those in which Gly9 is repaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met. Mutants (see AAW26371-90) of Rs- AFP2 are specifically claimed. The mutants show improved salt tolerant antifungal activity, particularly 136 80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG Triridericirirea Accaeca a regio de a accae a a como como a TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCCAGCTCACAAATGTATTTGTTA redesacarecresesacresesacianas de la redesación de la rede 6 Arragidarcardadriaderridecarccardadecacritringergererrer New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents. Gaps Rs-AFP1; radish antifungal protein 1; fungicide; salt tolerance; preservative; transgenic plant; crop protection. .. .. Score 178.8; DB 2; Length 414; Pred. No. 1e-46; 0; Mismatches 37; Indels 3; Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other; 'ttag= a 'trans1 except= (pos:85. .87, aa:Glu) 16. 102 \*ttag= b /\*tag= c Rees SB; Location/Qualifiers Disclosure; Fig 2; 39pp; English De Samblanx GW, 96WO-GB003065 95GB-00025474 Query Match 62.5%; Best Local Similarity 84.3%; Matches 214; Conservative CTTCCCATGTTAAT 270 Crrrccrrcrrahr 259 . .258 when expressed in plants WPI; 1997-332785/30. (ZENE ) ZENECA LTD. Raphanus sativus P-PSDB; AAW19617 Broekaert WF, 12-DEC-1996; WO9721814-A1 13-DEC-1995; 19-JUN-1997 sig\_peptide mat\_peptide 99 137 126 197 186 257 246 ద g 셤 g ò à ਨੇ à

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79 65 125

256

RESULT 11 AAZ39124

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The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence encodes a Butrema wasabi (Wasabia japonica) gamma-thionin protein from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TITGAAGCACCATCAATGGTGGAAGCGCAGAAGTTGTGTGCGAGAAGTCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TCAGGAGTCTGTGGAAACAACAATGCGTGCAAGAATCAGTGCATCAACCTTGAGGGAGCA 180
                                                                  Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CGACATGGATCTTGCAACTATATCTTCCCATATCACAGATGTATCTGTTACTTCCCATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 GAACACGGAICTIGCAACTAIGICTICCCAGCTCACAAAIGTATITGTTACTICCCAIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                            A disease-resistant plant in which wasabi gamma-thionin gene is introduced, creation of the disease-resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 177.4; DB 6; Length 243; Pred. No. 2.2e-46; 0; Mismatches 31; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 243 BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other;
                                 Wasabia japonica gamma-thionin encoding cDNA SEQ ID
                                                                                                                                                 Location/Qualifiers
1. .243
/*tag= a
/product= "gamma-thionin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 8; 11pp; Japanese.
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ilarity 86.0%;
Conservative (
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P-PSDB; ABP53725.
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Les 209; Conserv
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                                                                                                                    Eutrema wasabi
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes an antibacterial protein isolated from Wasabia japonica. The antibacterial protein can be used as a food or feed additive. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAGGAGTITGTGGGAACAACAATGCATGCAGGAACCAATGCAGAAACCTTGAAAGAGCA 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An antibacterial protein gene of Wasabia japonica - useful as a food-feed-additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                 Wasabia japonica antibacterial protein encoding cDNA SEQ ID NO:3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416;
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Pred. No. 1.6e-46;
0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 416 BP; 111 A; 77 C; 81 G; 147 T; 0 U; 0 Other;
                                                                                                                                                Wasabia japonica; antibacterial; food additive; ds.
                                                                                                                                                                                                                            1. .243 '-
/*tag= a
/product= "antibacterial protein"
 ВР.
 CDNA to mRNA; 416
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                                                                                                                                                                                                              Location/Qualifiers
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Best Local Similarity 83.9%;
Matches 214; Conservative
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                                                                (revised)
(first entry)
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Best Local Similarity
standard;
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                                                              15-SEP-2003
01-MAR-2000
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                                 AAZ39124;
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 AAZ39124
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Query Match
Best Local Similarity 83.5
Matches 213; Conservative
                                                                                                                                                                       Arabidopsis thaliana.
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Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 IGGGACATGGTCAGGAGTTTGTGGAACAACAATGCATGCAGGAACCAATGCAGAAACCT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 AATAATCATCATGAGGTAAGTTTGCTTCCATCATCACCACTTATCTTGGCTGCTGTTGTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes the Arabidopsis PDF1.2 gene which is used in a
                                                                                                                                                                  Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.6%; Score 176.2; DB 2; Length 400; 83.8%; Pred. No. 6.7e-46; ive 0; Mismatches 38; Indels 3
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/product= "PDF1.2"
/note= "plant defensin"
                                                                                                                                                                                                                                                 Location/Qualifiers
32. .274
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                                     AAV10633 standard; DNA; 400
                                                                                                   (first entry)
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/*tag= b
120. 271
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Matches 212; Conservative
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                                                                                                                                                                                                               Arabidopsis thaliana.
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                                                                                                                                  A. thaliana
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                                                                                                                                                                                   fungi; ss
                                                                   AAV10633;
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   RESULT 14
AAV10633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence encodes the Arabidopsis PDF1.1 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
                                                                                                                                                                                                                                                                                                                                                                                                                                         Manners JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 AAACAATAGTCATGGCTAAGTCTGCTACCATCGTTACTCTTTTCTTCGCTGCTCTTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Terras FRG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.7%; Score 176.6; DB 2; Length 83.5%; Pred. No. 5e-46; Live 0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Penninckx IAMA,
                                                                                                                                                                                                                                         /note= "plant defensin"
                                                                                                                                                                          /*tag= b
114. .265
/*tag= c
/product= "PDF1.1"
                                                                                                             Location/Qualifiers
26. .268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 1; 72pp; English
                                                                                                                                                                                                                                                                                                                                         97WO-GB001672
                                                                                                                                                                                                                                                                                                                                                                      96GB-00013753
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                                                                                                                                          /*tag= a
26. .113
/*tag= b
A. thaliana PDF1.1 DNA
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TGAAAGAGCAGAACCAGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence encodes a Butrema wasabi (Wasabia japonica) gamma-thionin protein from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 TITGAAGCACCAACAATGGTGGATGC---AAGGTTGTGCGAGAGACCAAGTGGGACATGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 TCAGAGTTTGTGGGAACAATGCATGCAGGAACCAATGCAGAAACCTTGAAAGAGC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 GAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAATGTATTTGTTACTTCCCATGT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09
                                                                                                                                                                                                                                     Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 AIGGCIAAGITIGCIACCAICACTICICITITICICIGCIGCICTITICITICTITIGCIGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A disease-resistant plant in which wasabi gamma-thionin gene is introduced, creation of the disease-resistant plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 175.8; DB 6; Length 243;
Pred. No. 7.2e-46;
0; Mismatches 32; Indels 3.
                                                                                                                                                                                                              Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 243 BP; 59 A; 55 C; 55 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .243
/*tag= a
/product= "gamma-thionin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 8-9; 11pp; Japanese.
                                                                                                                                       BP.
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85.6%;
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                                                CTTCCCATGTTAA 269
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Best Local Similarity 85.67
Matches 208; Conservative
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P-PSDB; ABP53726.
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                                                                                                                                                                                                                                                                           Eutrema wasabi.
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Db 181 CGACATGGATCTTGCAACTATATCTTCCCATATCTGTTACTTCCCATGT 240

Qy 267 TAA 269

Db 241 TAA 243

Search completed: May 18, 2004, 17:22:39

Job time: 280.85 secs
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COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
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US-08-627-706-12
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                                                                      May 18, 2004, 17:08:11 ; Search time 58.5 Seconds (without alignments) 2713.093 Million cell updates/sec
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                                                                                                                                                 1 gggaattcggatccaagaaa...........taataaggatccgaattccc 286
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Sequence 14,
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Sequence 9,
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Sequence 48
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*

(cgn2_6/ptodata/2/ina/5B_COMB.seq:*

(cgn2_6/ptodata/2/ina/6A_COMB.seq:*

(cgn2_6/ptodata/2/ina/6B_COMB.seq:*

(cgn2_6/ptodata/2/ina/6B_COMB.seq:*

(cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-103-489-12
US-09-103-489-12
US-09-103-489-14
US-09-103-489-14
US-09-103-489-14
US-09-103-489-9
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US-08-107-981-16
US-08-107-981-16
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                                                                                                                                                                                                            682709 segs, 277475446 residues
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                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               nucleic search, using sw model
                                                                                                                                                                        IDENTITY NUC Gapext 1.0
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Maximum DB seq length: 200000000
                                                                                                                      Title: . US-10-681-972-12 Perfect score: 286
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Match Length
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269.2
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172.2
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ö Sequence 50, A Sequence 50, A Sequence 50, Ap Sequence 50, Ap Gaps Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seguence Sequence Seguence 0; Sequence 12, Application US/08627706
Patent No. 5773696
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F STREET: 700 Chesterfield Village Parkway No. 5773696th CITY: St. Louis STATE: Missouri COUNTRY: USA 0; Indels MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPPRATING SYSTEM: PC-DOS/NS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/627,706 Query Match
100.0%; Score 286; DB 1;
Best Local Similarity 100.0%; Pred. No. 9.2e-84;
Matches 286; Conservative 0; Mismatches 0; US-08-627-706-8
US-09-103-489-8
US-08-377-687-50
US-08-377-687-50
US-08-777-192-50
US-08-971-982-50
US-08-627-706-11
US-08-133-6
US-08-137-687-31
US-08-137-687-31
US-08-177-192-31
US-08-777-192-31
US-08-777-192-31
US-08-977-192-31
US-08-977-192-31
US-08-977-192-31
US-08-977-192-31 CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: COhen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 34,565
TELEPHONE: (314)537-6224
TELEPHONE: (314)537-6047
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single ALIGNMENTS 3306 3306 3306 2284 40 284 40 40 1150 1150 1150 1150 1111.6 1111.6 1111.6 76.8 76.8

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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: W. Younie S.
APPLICANT: W. Younie S.
APPLICANT: W. Younie S.
APPLICANT: Wosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C.
CURRENT APPLICATION NUMBER: US/09/829,38LD
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
         61 TCTTTGCTGCTCTTGTTCTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCAAGGT 120
                                                                                                                                           TCTTTGCTGCTCTTGTTCTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 ACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTC
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                                                                                                                                                                                            241 ACANATGTATTTGTTACTTCCCATGTTAATAAGGATCCGAATTCCC 286
                                                                                                                                                                                                                     241 ACAAATGTATTTGTTACTTCCCATGTTAATAAGGATCCGAATTCCC 286
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                                                                                                                    181 ACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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// OTHER INFORMATION: Synthetic PCR reaction product

US-09-829-381D-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 9.2e-84;
Matches 286; Conservative 0; Mismatches 0;
                                              121 TGTGCGAGAGCCAAGTGGGACATGGTCAGGAGTTTG
                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09829381D Patent No. 6653280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 14, Application US/08627706; Patent No. 5773696; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      US-09-829-381D-12
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LENGTH: 286
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1 GGGAATTCGGATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTTC 60
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                                                                         61 refriréciécretriferretrirecrecerritérasecaceacaargergeargea
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                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenie S.
ADDRESSEE: Charles E. Cohen, Monsanto Company. BR4F
                                                                                                                                                                                                                                                                                     241 ACAAATGTATTGTTACTTCCCATGTTAATAAGGATCCGAATTCCC 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Charles E. Cohen, Monsanto Company, BB4F
700 Chesterfield Village Parkway No. 6215048th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 286; DB 3;
100.0%; Pred. No. 9.2e-84;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09103489
Patent No. 6215048
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Best Local Similarity 100.0
Matches 286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
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CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
              NUMBER OF SEQUENCES:
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                                                                  STREET: 700 Chest
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonile S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                     COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: COhen, Charles E:
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700)A
TELECOMMUNICATION INFORMATION:
TELECHONE: (314)537-624
TELECHONE: (314)537-624
TELEFRAX: (314)537-624
INFORMATION POR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 ATTIGITACTICCCAIGITAATAAGGAICC 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
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Sequence 14, Application US/09829381D
Patent No. 6653280
Patent No. 6653280
Patent No. 6653280
Patent No. 6653280
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Clindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: COMEN. Charles E.

REGISTRATION NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 34.565
TELEPHONE: (314) 537-6047
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 94.1%; Score 269.2; DB 3; Best Local Similarity 99.3%; Pred. No. 2.7e-78; Matches 268; Conservative 2; Mismatches 0;
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                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: single
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mall male man

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Floppy disk
                                                                                                                               Query Match
Best Local Similarity 91.69
Matches 241; Conservative
           500 base pairs
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                          TYPE: nucleic acid
STRANDEDNESS: single
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TYPE: nucleic acid
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                                                             ; TOPOLOGY: linear; MOLECULE TYPE: CDNAUS-08-627-706-9
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STRANDEDNESS:
TOPOLOGY: lin
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US-09-103-489-9
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             LENGTH:
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Patent No. 5733696
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
STATE: Wissouri
                                                                                                                                                                                                                                                                          9 GGATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTTCT
                                                                                                                                                                                                 94.1%; Score 269.2; DB 4; Length 270; 99.3%; Pred. No. 2.7e-78; tive 2; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ATTIGITACTICCCAIGITAATAAGGAICC 270
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: COhen, Charles B.
REGISTRATION NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 270
                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (314)537-6224
TELEPAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 9;
SEQUENCE CHARACTERISTICS:
                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Plasmid
US-09-829-381D-14
                                                                                                                                                                                               Query Match
Best Local Similarity 99.3:
Matches 268; Conservative
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CLASSIFICATION: 436
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                                                                                                                                                       3; Gaps
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APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Wu, Yonnie S.
APPLICANT: Wu, Yonnie S.
ITILE OF INVENTION: Antifungal Polypeptide and Methods for
ITILE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles B. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: K. Louis
STATER: Missouri
                          Length 500;
75.7%; Score 216.6; DB 1; Length 91.6%; Pred. No. 5e-61; Live 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DAYE: 24-JUN-1998
CURSSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REFERENCE/DOCKET NUMBER: 34-565
REFERENCE/DOCKET NUMBER: 34-565
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 TATTIGITACTICCCAIGITAAT 312
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Patent No. 6215048
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230 CAGAAACCTIGAAAGAGCAGAACACGGATCTIGCAACTAIGICTICCCAGCTCACAAAIG 289
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APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
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ZIP: 63196
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
ATCHASTIFICATION: 436
ATCHASTIFICATION: A34,565
FREGISTRATION NUMBER: 34,565
FREGISTRATION NUMBER: 38-21(10700)A
FELENCOMMUNICATION NUMBER: 38-21(10700)A
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                                                                                                                               248 TATITGITACTICCCATGITAAT 270
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Patent No. 5773696
GENERAL INFORMATION:
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STRANDEDNESS: single
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Plant Pathogenic Fungi
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR PILING DATE: 2001-04-09
PRIOR PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                       Gaps
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                                                                                                               tch 75.7%; Score 216.6; DB 3; Length 500; al Similarity 91.6%; Pred. No. 5e-61; 241; Conservative 0; Mismatches 19; Indels 3
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ORGANISM: Alyssum spp
; MOLECULE TYPE:
US-09-103-489-9
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                                                                                                               Query Match
Best Local
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Query Match
Best Local Similarity 86.1
Matches 223; Conservative
                                                                   GENERAL INFORMATION:
                        US-09-829-381D-5
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US-08-377-687-48
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LENGTH: 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 308;
                                                                                    Sequence 5, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Idan, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
                                                                                                                                                                                                                                                              E: Charles E. Cohen, Monsanto Company, BB4F
700 Chesterfield Village Parkway No. 6215048th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC comparible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 190.8; DB 3;
Pred. No. 1e-52;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTONEY FACETATION: OUN ATTONEY FACETATION: NAME: COhen, Charles E. REGISTRATION NUMBER: 34,565
REPERENCE/DOCKET NUMBER: 38-21
TELEPHONE: (314) 537-624
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 308 base pairs
TYPE: nucleic acid
290 CATATGCTACTTCCCCTGT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 TATTIGTTACTICCCATGT 266
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Best Local Similarity 86.1%;
Matches 223; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Younie S.
APPLICANT: Wu Younie S.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: Plant Pathogenic Fungi
CURRENT APPLICATION NUMBER: 10700, C
CURRENT FILING DATE: 2001-04-09
PRIOR PILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
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86.1%; Pred. No. 1e-52;
Live 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Synthetic PCR reaction product
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Patent No. 5538252
GENERAL INFORMATION:
APPLICANT: BROBKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN DARBY & CUSHWAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: (22)..(248)
; FURR INFORMATION: N = any nucleotide
US-09-829-381D-5
Sequence 5, Application US/09829381D Patent No. 6653280
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SOFTWARE: PatentIn version 3.1
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STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C.
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US-08-777-192-48
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US-08-971-982-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 TITIGCIGCITICGAAGCACCAACAAIGGIGGAAGCACAGAAGITIGIGGGAAAGGCCCAAG
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                                                                                                                                                                                                  CLASSIFICATION: 800
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KONULLS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: ANAMACTERISTICS:
FENCHALION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48, Application US/08777192
Patent No. 5824669
GENERAL INFORMATION:
APPLICANT: BROBKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBOOKN, RUPERT W.
APPLICANT: OSBOOKN, RUPERT W.
APPLICANT: TERRAS, SARAH B.
APPLICANT: TERRAS, SARAH B.
TITLE OF INVENTION: BIOCIDAL PROTEINS
ITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CUSHMAN DARBY & CUSHMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 84.3
Matches 214; Conservative
                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: 16..255
US-08-377-687-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
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US-08-777-192-48
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80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACAAG 136
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                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION NUMBER: 99042/SEE.36525/US/A
TELECHONE: 202-861-3000
TELEPRAX: 202-82-994
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.5%; Score 178.8; DB 1;
84.3%; Pred. No. 9.7e-49;
Live 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/08971982
Fatent No. 6187904
GENERAL INFORMATION:
APPLICANT: BROEKABRT, WILLEM F.
CAMMUE, BRUNO P.A.
OSBORN, RUPERT W.
REES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLEYDEN, JOZZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
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Matches 214; Conservative
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80 CITIGCIGCCITIGAAGCACCAACAAIGGIGGAIGCA---AGGITGIGCGAGAGACCAAG 136
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; LOCATION: 16..255
; SEQUENCE DESCRIPTION: SEQ ID NO: 48;
US-08-971-982-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCCCATGTTAAT 270
                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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Search completed: May 18, 2004, 19:02:18 Job time : 59.5 secs Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 21, Appl Sequence 8, Appli Sequence 8, Appli Sequence 50, Appli Sequence 50, Appli Sequence 283, Appli

Sequence 2046, Ap Sequence 2046, A Sequence 16, Appl

Sequence 15, Appl Sequence 13, Appl Sequence 21, Appl Sequence 17, Appl Sequence 46, Appl

9 US-09-759-584-58 9 US-09-938-842A-2046 9 US-09-938-842A-2046 9 US-09-829-381A-16 13 US-10-681-972-17 19 US-09-829-381A-17 19 US-09-732-561-21 9 US-09-732-561-21 9 US-09-732-561-21 10 US-10-681-972-16 9 US-09-732-561-21 10 US-10-681-972-8 11 US-10-178-449A-11 12 US-10-178-449A-11 13 US-10-178-449A-11 14 US-10-178-449A-11 15 US-10-178-449A-11 16 US-10-178-449A-11 17 US-10-178-449A-11 18 US-10-178-449A-11 19 US-10-178-449A-11 10 US-10-178-449A-11 11 US-10-178-449A-11 12 US-10-178-449A-11 13 US-10-178-449A-11 14 US-10-178-449A-11 15 US-10-178-449A-11 16 US-10-178-449A-11 17 US-10-178-449A-11 18 US-10-178-449A-29 19 US-10-178-449A-31 19 US-10-178-449A-31

Sequence 9, Appli Sequence 19, Appl Sequence 23, Appl Sequence 6, Appli Sequence 11, Appl Sequence 88, Appl Sequence 29, Appl Sequence 48, Appl Sequence 48, Appli Sequence 48, Appli Sequence 48, Appli Sequence 48, Appli Sequence 31, Appli

Sequence 11, App.

US-09-829-381A-11 US-10-681-972-11

ALIGNMENTS

Sequence 34, Sequence 11, Seguence

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ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "", "Experience Cindy A. Rosenberger, Cindy A. Rosenberger, Cindy A. TITLE OF INVENTION: Antifungal Polypeptide and Methods Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

CONFUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRINT APPLICATION DATA:

APPLICATION NUMBER: US/09/829,381A

FILING DATE: 09-Apr-2001

CLASSIFICATION: GUNCOMD>

PRIOR APPLICATION: GUNCOMD>

PROFICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNAY AGENT INFORMATION:

NUMBER: OFFICE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO
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REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                US-09-829-381A-12
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Sequence 12, Appl
Sequence 14, Appl
Sequence 14, Appl
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Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
                                                                                                   May 18, 2004, 17:59:12 ; Search time 263.25 Seconds (without alignments) 4930.226 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-006-252A-19
US-09-732-561-13
US-09-732-561-15
US-09-887-576-607
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US-09-829-381A-14
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US-09-829-381A-9
3 US-10-681-972-9
US-09-829-381A-5
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                                                                                                                                                                                                                                                                                   2947324 seqs, 2269024515 residues
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US-09-759-584-48
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                                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                181 ACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTC
             61 TCTTTGCTGCTCTTGTTCTCTTTGCTGCCTTTTGAAGCACCAACAAAGATGGAAGGT
                                                                                            181 ACCAAIGCAGAAACCTIGAAAGAGCAGAACACGGATCTIGCAACTAIGICTTCCCAGCTC
                                                                                                                                  9 GGATCCAAGAAAGTAATAGATATGCTAAGTTTGCTACCATCATCTCTTTTTTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 38-21 (10700) A TELECOMMUNICATION INFORMATION: TELEPHONE: (314) 537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-829-381A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: COhen, Charles E.
REGISTRATION NUMBER: 34,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 270 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-829-381A-14
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Best Local
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Sequence 12, Application US/10681972

Publication W. US20040064850A1

Publication W. US20040064850A1

Publication W. US20040064850A1

APPLICANT: Liang, Jihong

APPLICANT: Liang, Jihong

APPLICANT: Stah, Dallip M.

APPLICANT: W. Yonnie S.

APPLICANT: W. Yonnie S.

APPLICANT: W. Yonnie S.

APPLICANT: W. Yonnie S.

APPLICANT: W. Yonnie S.

APPLICANT: W. Yonnie S.

APPLICANT: W. Yonnie S.

APPLICANT: W. Yonnie S.

APPLICANT: W. Yonnie S.

CURRENT: W. Yonnie S.

APPLICANTON WUBBR: US/00/829,381D

PRIOR APPLICATION NUMBER: US/09/829,381D

PRIOR PRIOR PRIOR DATE: LOS US/01/03/489

PRIOR APPLICATION NUMBER: US/09/103,489

PRIOR APPLICATION NUMBER: US/09/103,489

PRIOR APPLICATION NUMBER: US/09/103,489

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PRIOR APPLICATION NUMBER: US/09/103,489
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100.0%; Score 286; DB 13;
Best Local Similarity 100.0%; Pred. No. 8.7e-83;
Matches 286; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                            100.0%; Score 286; DB 9;
100.0%; Pred. No. 8.7e-83;
iive 0; Mismatches 0;
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                                                                                                                                                             ;
TOPOLOGY: linear
;
MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-829-381A-12
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCCAGCTCACAAATG 247
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                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSER: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 Arcacagaaagraafagararggcraagrefecrrccarcarcrccrrgrcrecrecr
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                                                                          Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 61198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: ASYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION TUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 ATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTT
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Pred. No. 5e-60;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cohen, Charles E. REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATITGTTACTICCCATGITAAT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 9, Application US/10681972
; Publication No. US20040064850A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 500 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                          APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.7
Best Local Similarity 91.6
Matches 241; Conservative
                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                         CITY: St. Louis
STATE: Missouri
            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-829-381A-9
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US-10-681-972-9
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APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contro;
TITLE OF INVENTION: Altifungal Polypeptide ALYAFP from Alyssum and Methods for Contro;
TITLE OF INVENTION: Altifungal Polypeptide ALYAFP from Alyssum and Methods for Contro;
TITLE OF INVENTION: Altifungal Polypeptide ALYAFP from Alyssum and Methods for Contro;
FILE REFERENCE: 38-21 (10700) C
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR PELLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Version 3.1
SEQ ID NO 14
IENGTH: 270
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                      GCTCTTGTTCTTTTGCTGCCTTTGAAGCACCAACAATGCTGGATGCAAGGTTGTGCGAG 120
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                                                                                              181 AGAAACCTTGAAAGAGGAGAACAGGAATCTTGCAACTATGTCTTCCCAGCTCACAAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGT
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Pred. No. 2.6e-77;
2; Mismatches 0; Indels
                                                                                                                                                                                                                   ATTIGITACTICCCAIGITAATAAGGAICC 278
                                                                                                                                                                                                                                         ATTTGTTACTTCCCATGTTAATAAGGATCC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 ATTIGITACTICCCAIGITAATAAGGATCC 278
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; Sequence 14, Application US/10681972
; Publication No. US20040064850A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09829381A Patent No. US20020144306A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.3%;
Matches 268; Conservative
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; OTHER INFORMATION: Plasmid
US-10-681-972-14
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Sequence 5, Application US/10681972
; Sequence 5, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:
APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Shah, Dilip M.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; TITLE OF INVENTION: Plant Pathogenic Fungi
; TITLE OF INVENTION: Diant Pathogenic Fungi
; TITLE OF INVENTION: Diant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; PRIOR APPLICATION NUMBER: US/09/829,381D
; PRIOR PELING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTHARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 190.8; DB 9; Length 86.1%; Pred. No. 1e-51; Live 0; Mismatches 33; Indels
                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apx-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                            NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-829-381A-5
                                                                                                                                                                                                                                                                                                                        TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 223; Conservative
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Best Local Similarity
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                                           APPLICANT: Wu, Yonnie S.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contror TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C.
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR PLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTGTTCTCTTTGCTGCCTTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 Arcacadaaadraaradararddcraachdrachrocarcarchochdrachdcrad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCCAGCTCACAAATG
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APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 216.6; DB 13; Length 500;
Pred. No. 5e-60;
0; Mismatches 19; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature; LOCATION: (22)...(22); OTHER INFORMATION: N = any nucleotide US-10-681-972-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATITGITACTICCCATGITAAT 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.6%;
Matches 241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 63198
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Alyssum spp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-829-381A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
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Gaps 3; 79 65 136

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66 TITIGCIÈCITICGAAGCACCAACAATGGTGGAAGCACAGAAGTIGTGCGAAAGGCCAAG 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 TGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAGTGTATCTGCTA 245
                                                                                                                                                                                                                                                                                                                                                                                              80 CITITGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 414;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                       62.5%; Score 178.8; DB 9;
84.3%; Pred. No. 9.7e-48;
live 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE KEFEAGULE. 3003-FEDULE.

CURRENT APPLICATION NUMBER: US/10/388,361A

CURRENT FILING DATE: 2003-03-13

PRIOR APPLICATION NUMBER: US 09/077,948

PRIOR FILING DATE: 1998-08-07

PRIOR FILING DATE: 1996-12-12

PRIOR FILING DATE: 1996-12-12

PRIOR FILING DATE: 1996-12-13

PRIOR FILING DATE: 1996-03-28

PRIOR FILING DATE: 1995-12-13

NUMBER: OF SEQ ID NOS: 141

SEQ ID NO 45

LENGTHA. 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Broekaert, Willem
APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: 50094PPDDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45, Application US/10388361A Publication No. US20030226169A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Puijk, Wouter
Schaaper, Wilhelmus
Broekaert, Willem
Van Gelder, Wilhelmus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borremans, Frans
De Samblanx, Genoveva
Sitjtsma, Lolke
Meloen, Robbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Van Amerongen, Aart
APPLICANT: Fant, Franky
         INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 CTTCCCATGTTAAT 270
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Best Local Similarity 84.3
Matches 214; Conservative
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; ORGANISM: Raphanus sativus
US-10-388-361A-45
202-822-0944
                                                                                                                                                                    CDS
16..255
                                                                                                                                                                ; NAME/KEY;
; LOCATION:
US-09-759-584-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-388-361A-45
TELEFAX:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                       CAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATG 247
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                  Length 308;
                                                                                                                                                                          Score 190.8; DB 13; Length
Pred. No. 1e-51;
0; Mismatches 33; Indels
                                                                                                                                                                                                                                                       11 ATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
   ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic FCR reaction product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION UNBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDELEXDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CADDRESSEE: CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                           FEATURE:

NAME/KEY: misc feature

LOCATION: (22)...(248)

OTHER INFORMATION: N = any nucleotide
US-10-681-972-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 48, Application US/09759584
Patent No. US20010014732A1
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMWUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 TATTTGTTACTTCCCATGT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 chraicchachtecerer 308
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Best Local Similarity 86.1%;
Matches 223; Conservative
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COUNTRY: US.
ZIP: 20005
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US-09-759-584-48
                                                                                                                                                                      Query Match
Best Local S
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246 CTTTCCTTGTTAAT 259

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79 TCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 ITGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTT 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
                                              Sequence 13, Application US/09732561

Fatent No. US20020035738A1

GENERAL INFORMATION:
APPLICANT: Thorma, Bart
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Razan, Kemal
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA AG Products
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
61.7%; Score 176.6; DB 9;
Best Local Similarity 83.5%; Pred. No. 5e-47;
Matches 213; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR ADDICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 37.712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ARDIGA APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                   80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 136
                                                                                                                                                                                                                                               66 ritigciectirceaagcaccaacaarderegaagcacagaagricheggaaaggccaag 125
                                                                                                                                                                                                                                                                                                   TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA 256
                                                                                                                                                         65
                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 TGAGAAAGCACGACATGCATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTA 245
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                                                                                                                                                 6 ATTAGTGATCATGGCTAGGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCT
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                                                         Gaps
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Query Match 62.5%; Score 178.8; DB 13; Length 414; Best Local Similarity 84.3%; Pred. No. 9.7e-48; Matches 214; Conservative 0; Mismatches 37; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%; Score 178.8; DB 14; Length 414; 84.3%; Pred. No. 9.7e-48; ive 0; Mismatches 37; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                **Sequence 19, Application US/10006252A

**Publication No. US20020152498A1

**GEMERAL INFORMATION:

**APPLICANT: De Samblaux, Genoveva

**APPLICANT: Brockaert, Willem

**APPLICANT: Rees, Sarah

**ITLE OF INVENTION: Antifungal Proteins

**FILE REPERENCE: SYN-034DV

**FILE REPERENCE: SYN-034DV

**CURRENT APPLICATION NUMBER: US/10/006,252A

**CURRENT FILING DATE: 2001-12-04

**PRIOR APPLICATION NUMBER: 09/077,951

**PRIOR APPLICATION NUMBER: QB 9525474.4

**PRIOR APPLICATION NUMBER: PCT/GB96/03065

**PRIOR APPLICATION NUMBER: PCT/GB96/03065

**NUMBER OF SEQ ID NOS: 77

**SOFTWARE PATENT OF THE TOWN TOWER: PCT/GB96/03065

**SOFTWARE PATENT OF THE TOWN TOWER: PCT/GB96/03065

**SOFTWARE PATENT OF THE TOWN TOWER: PCT/GB96/03065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 CITCCCATGITAAT 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Raphanus sativus
US-10-006-252A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.5
Best Local Similarity 84.3
Matches 214; Conservative
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US-10-006-252A-19
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LENGTH: 414
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202 TGAAGGAGCCAAACATGGATCATGCAACTATGTCTTCCCAGCACACAGTGTATCTGTTA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 |
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APPLICANT: Brown, D.
APPLICANT: Chang, H.
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APPLICANT: Chang, H.
APPLICANT: Han, B.
APPLICANT: Wang, X.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1260.001051
CURRENT APPLICATION NUMBER: US 60/213,848
FILE RAPLICATION NUMBER: US 60/213,848
FRICH APPLICATION NUMBER: US 60/214,087
FRICH APPLICATION NUMBER: US 60/214,087
FRICH SPLING DATE: 2000-06-23
FRICH APPLICATION NUMBER: US 60/228,692
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61.6%; Score 176.2; DB 9;
Best Local Similarity 83.8%; Pred. No. 6.7e-47;
Matches 212; Conservative 0; Mismatches 38;
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Patent No. US20020144047A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or
US-09-887-576-607
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Pred. No. 6.7e-47;
0; Mismatches 38; Indels 3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/09732561
Fatent No. US20020035738A1
Fatent No. US20020035738A1
FAPELICANT: Thomma.
APPLICANT: Thomma.
APPLICANT: Perras, Franky
APPLICANT: Manners, John
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
APTIONS DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
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ADDRESS:
SIREET: ZENECA AG Products
CITY: Wilmington
STATE: DECOUNTRY: Tree
ZIP:
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Matches 212; Conservative
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STRAIN: PDF1.2
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US-09-732-561-15
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                                           APPLICANT: BROBKAERT, WILLEM F.
APPLICANT: CARWID: BRUNO P.A.
APPLICANT: CARWID: BRUNO P.A.
APPLICANT: CARWID: BRUNO P.A.
APPLICANT: CARWID: BRUNO P.A.
APPLICANT: CARWID: REES, SARAH B.
APPLICANT: REES, SARAH B.
APPLICANT: REES, SARAH B.
APPLICANT: REES, SARAH B.
APPLICANT: RERAS, FRANKY R.G.
APPLICANT: VANDELEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEGURNESS:
ADDRESSE: CUSHWAN DARBY & CUSHWAN
STREFT: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
CONNTRY: USA
ZIP: D.C.
CONPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PARCHITIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FLING DATE:
APPLICATION NUMBER: 08/377,687
FILING DATE:
APPLICATION NUMBER: 08/377,687
FILING DATE:
APPLICATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
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REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 208-861-3000
TELLEPHONE: 20-861-3000
Sequence 58, Application US/09759584
Patent No. US20010014732A1
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US-09-759-584-58
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Search completed: May 18, 2004, 20:33:21 Job time : 264.25 secs

us-10-681-972-12.rst

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May 18, 2004, 17:05:11; Search time 2381.6 Seconds (without alignments) 3586.070 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES ΩÏ Ouery Match Length DB Score

BG32151 D501 08a0 BG321515 D501 08a0 CD8345 25-E8974-CD834068 BN45.040H CD832592 BN40.0630

BG321515 CB263345 CD834068 CD832592

12 14 14 14

410 441 446 447

64.0 62.2 62.2 62.2

183 177.8 177.8 177.8

Result No.

Description

32071 BN40. 34994 BN45. 31680 BN40. 21454 DS01. 7956 AV7879	000000000000000000000000000000000000000	111014 BN40. 1118 ATTS194 5118 ATTS194 52525 BV486 52625 BN40. 4168 BN45. 4108 BN45. 4108 BN45. 4108 BN45. 4107 BN45. 11972 BN45. 11972 BN40. 83048 BN40.	7568 BN45.052 7568 BN45.052 7692 BN45.040 7692 BN45.040 7824 BN45.040 7824 BN40.058 7832 BN40.058 784 AV789144
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## ALIGNMENTS

EST 27-FEB-2001 Seedlings ince.	ophyta; ; N.A.	, Kla
EST 27-   seedlin	/ Trache eudicots curainia is,L.J., d Tinker nia soph	Ontario
linear Flixweed nRNA segu	oryophyta 1s; core 1eae; Des A., Harr Ott, D. an	Ottawa,
mRMA stressed _08a06, n	lyta; Emb Sotyledon Brassicac De Moors, S., Spro	n Centre cal Farm,
10 bp RC cold s	Streptoph ta; eudic icales; E oux,P., I Robert,L.	Research Canada xperiment
AAFC ECO	llantae; moliophy I; Brass (C., Cour let,T., l	. oilseed ri-food (entral E) 2 1 agr.ca.
R Ds01_ la sophia [ GI:131	viridip Viridip Viridip Vyta, Mag Virosids I 1 to 410 , Piche, I., Ouel Sequence	td (2001) ingh, J.B. ireal and e and Age Bldg., C 159-166 759-170
BG321515  410 bp mRNA linear EST 27-FEE DS01_08a06_R DS01_AAFC_ECORC_cold_stressed_Flixweed_seedlings BG321515 BG321515.1 GI:13151193 EST.	Descurainia sophia Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Descurainia. 1 (bases 1 to 410) Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A. Expressed Sequence Tags from Cold-Stressed Descurainia sonbia	Seedlings Unpublished (2001) Contact: Singh,J.A. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-food Canada RW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, OC6, Canada Tel: (613) 759-1662 Eax: (613) 759-1601 Email: singhja@em.agr.ca.
RESULT 1 BG321515 LOCUS DEFINITION ACCESSION VERSION SERVORDS SOURCE	ORGANISM REFERENCE AUTHORS TITLE	JOURNAL

ORIGIN

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/ tissue_Lype="seedling"
/ (dev_stage="few_days old seedlings"
/ (lab_host="E. coli_XL1-Blue MRF"
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/ (host="Vercor: pallescript SK (-); Site 1: EcoRI; Site 2:
/ (host="Vercor: pallescript SK (-); Site 1: EcoRI; Site 2:
/ (host="Vercor: pallescript SK (-); Site 1: EcoRI; Site 2:
/ (host="Vercor: pallescript SK (-); Site 1: EcoRI; Site 2:
/ (host="Vercor: pallescript SK (-); Site 1: EcoRI; Site 2: Sequencing granted in Planck-Institute for Plant Breeding Research, Cologing Granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity,
/ Establishment of high-efficienty SRP-based mapping tools and development of methods for genome-wide mutation detection PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de This clone is available from RZPD; contact RZPD (clone@rzpd.de)
for further information."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD834068 446 bp mRNA linear EST 10-JUL-2003
BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA
sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

    (Dases 1 to 446)

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Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGAGACCAAG
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62.2%; Score 177.8; DB 14; Length
Best Local Similarity 84.2%; Pred. No. 6e-38;
Matches 213; Conservative 0; Mismatches 37; Indels
                                                        organism="Arabidopsis thaliana"
            Location/Qualifiers
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CD834068.1 GI:32516008
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                                    source
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DEFINITION
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                                                                                                                /clone="DB01_08a06"
/tissue_type="leaf, stem"
/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
/clone_lib="DB01_AAFC_ECORC_cold_stressed_Flixweed_seedlin
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25-E8974-008-017-A07-pB12 MPIZ-ADIS-008 Arabidopsis thaliana cDNA clone MPIZp767A0717Q 5-PRIME, mRNA sequence.
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Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)
                                                                                                                                                                                                                                 /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI; Site 2: Xho I; Plants were grown for 1 month at 200C/16 rise light/day (average 8 leaves, 1 cm tall, weight 0.02g/plant). Then they were exposed to 20C, 12 hrs light/day, for 1 week. Library prepared by C. Piche using Stratagene kit."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 TAGAGGGCACAACATGGATCTTGCAACTATGTCTTCCCAGCKCACAGTGTATATGTKAC 252
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                                                                                                                                                                                                                                                                                                                                                                                                                         ch 64.0%; Score 183; DB 12; Length 410; Il Similarity 81.0%; Pred. No. 2.2e-39; 205; Conservative 6; Mismatches 42; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Indels
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
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Fax: 00492215062851
                                                 organism="Descurainia sophia"
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Insert Length: 41 std Error: 0.00
Plate: 17 row: A column: 07
Seq primer: pBl2; GGTGGCGGCCGCTCTAG.
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                                                                    [_type="mRNA"
xref="taxon:89411"
    iocation/Qualifiers
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TITLE

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Gaps 3; 79 74 136 134 194 256 114 136

79

196 234

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EST 10-JUL-2003
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BN40.061003F011227 BN40 Brassica napus cDNA clone BN40061003, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                    TGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATTTGCTA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

Location/Qualifiers
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Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                             80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG
                                                                                                                                                                                                                                                                                                137 IGGGACAIGGICAGGAGITIGIGGGAACAACAATGCAIGCAGGAACCAAIGCAGAAACCI
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                                                                                            Length
                                                                                                                          37; Indels
                                                                                      Score 177.8; DB 14;
Pred. No. 6e-38;
0; Mismatches 37; ]
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84.2%; Pred. No. 6e-38;
Micmatches 37;
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                                                                                   Query Match
Best Local Similarity 84.2%;
Matches 213; Conservative
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Best Local Similarity
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CD832071
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                                                                                                                                                                                                                                                                                                                                                                                             256
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                           20 AGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTTTTTTTGCTGCTCTTTGTTCT 79
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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Unpublished (2003)
Contact: Genoplante
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                     Query Match
62.2%; Score 177.8; DB 14; Length 446;
Best Local Similarity 84.2%; Pred. No. 6e-38;
Matches 213; Conservative 0; Mismatches 37; Indels 3;
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/tissue_type="seed"

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CD832592.1 GI:32514532
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CD831680 470 bp mRNA linear EST 10-JUL-2003 BN40.060H13F011227 BN40 Brassica napus cDNA clone BN40060H13, mRNA
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DS01_08h05_A DS01_AAFC_ECORC_cold_stressed_Flixweed_seedlings
Descurainia sophia cDNA clone DS01_08h05, mRNA sequence.
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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 ACTAGTGAGCATGGCTAAGTTTGCTTCCATCATTGCCCCACTTTTTGCTGGTCTTGTTCT
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Brassica napus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"

cultivar="Jet neuf"

db_xref="texon:3708"

clone="BN40060H13"

tlissue type="seed"

clone_lib="BN40"
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CD831680.1 GI:32513620
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BG321454.1 GI:13151132
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Genoplante
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This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

1. .458

//organism=Brassica napus"
//mol type="mRNA"
//mol type="mRNA"
//cultivar="Jer neuf"
//db xref="taxon:3708"
//clone="EN45043006"
//tissue type="seeed"
//clone="EN45043006"
//clone="EN45043006"
                                                                                                                                                                                                                                                                                                                                                CD834994
BN45.043006F011229 BN45 Brassica napus CDNA clone BN45043006, mRNA
sequence.
                   120 TTTCGCTGCTTTCGAAGCACCAACATGGTGGAAGCACAGAAGTTGTGCAAGAGGCCAAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids, eurosids, eurosids II, Brassicales, Brassicaceae; Brassica.
CTITGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 136
                                                                                                                                            TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA 256
                                                                                                                                                                                     299
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                                                                    180 TGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAAACCT
                                                                                                                                                                               240 reaganagenegaenterigeaetrateretreceaetreaenentagen
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CD834994.1 GI:32516934
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Brassica napus
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Genoplante
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                                                                                                                                                                                                                                                           CTTCCCTTGTTAA 312
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Best Local Similarity 84.24
Matches 213; Conservative
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Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-960
Email: meski@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a Sstl/Khol insert. Please visit our further (http://www.gsc.riken.go.jp/e/plant/index_e.html) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T04323
370 Lambda-PRL2 Arabidopsis thaliana CDNA clone 37F10T7, mRNA
sequence.
                                                                                                                                    Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itch,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
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/dev stage="Plants at various developmental stages from germination to mature seeds"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10,
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/note="Site 1: SstI; Site 2: XhoI; subjected t dehydration (1, 2, 5, 10, 24 hr) and cold (1, hr) treatments"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db xref="taxon:89411"
/db xref="taxon:89411"
/clone="100108h05"
/tissue_type="l-faf, stem"
/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
/clone_lib="D801_AAFC_ECORC_cold_stressed_Flixweed_seedlin
Descurainia sophia
Descurainia sophia
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Descurainia.

1 (bases 1 to 394)
Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J.,
Bxpressed Sequence Tags from Cold-Stressed Descurainia sophia
Seqlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI; Site 2: Xho I; Plants were grown for 1 month at 200C/16 hrs light/day (average 8 leaves, 1 cm tall, weight 0.02g/plant). Then they were exposed to 2oC, 12 hrs light/day, for 1 week. Library prepared by C. Piche using Stratagene kit."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Singh,J.A.
Bastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
0.06, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: singhja@em.agr.ca.
Location/Qualifiers
1. .394
/organism="Descurainia sophia"
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Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (613) 759-1662
(613) 759-1701
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1 (bases 1 to 400)
Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,
McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,
Retzel, B. and Somerville, C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD833779 408 bp mRNA linear EST 10-JUL-2003 BN45.001115F010914 BN45 Brassica napus CDNA clone BN45001115, mRNA sequence.
CD833779 GI:32515719
EST.
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                                                                                                                                                        Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38; Indels
                                                                                                                                                                                                                                                             Email: 22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligo dT primed cDNA.
                                                                                                                                                                                                                                                                        Seq primer: T7 dye primer.
Location/Qualifiers
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                                                                                                                                                                                                                                  Tel: 517-353-0854
Fax: 517-353-9168
                                                                                                                                                                                                                    Lansing, Mi
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7846151
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409 bp mRNA linear EST 10-JUL-2003 BN45.040121F011018 BN45 Brassica napus cDNA clone BN45040121, mRNA BSGquence. CD834090 CD834090.1 GI:32516030
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Brassica napus (rape)
Brassica napus
Bukaryota, angus
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Tobids; eurosids II; Brassicales; Brassicaceae; Brassica.
Genoplante.
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(bases 1 to 409)
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                                                                                                                                                                                                          93, tue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante.info.infoblogen.fr).
                                                                                                                                     Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
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Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 61.6%; Score 176.2; DB 1.
Best Local Similarity 83.8%; Pred. No. 1.6e-37;
Matches 212; Conservative 0; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                      organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="RNA5001115"
/tissue_type="seed"
/clone_lib="BN45"
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Brassica napus
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ch 61.6%; Score 176.2; DB 1-
al Similarity 83.8%; Pred. No. 1.6e-37;
212; Conservative 0; Mismatches 38
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CD826491.1 GI:32508431
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 420)

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Contact: Genoplante
Genoplante
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         Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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                                                                                                                       /organism="Brassica napus"
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                                                                                          Location/Qualifiers
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BN25.064A05F020416 BN25 Brassica napus CDNA clone BN25064A05, mRNA
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Brassica napus
Brassica napus
Bukaryota, Viridplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II, Brassicales; Brassicaceae; Brassica.

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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
This sequence programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.ft).
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Genoplante, a major partnership french program in plant genomics
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Best Local Similarity 83.8%; Pred. No. 1.6e-37;
Matches 212; Conservative 0; Mismatches 38; Indels 3;
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OY  80 CITTGCTGCTTTGAAGCACCAACAATGGTGCAAGGTTGTGCGAGAGACCAAG 136  101 TTTCGCTGCTTCTCGAAGCACCAACAATGGTGGAAGACACGAAGTTGTGCGAGAGACCAAG 160  37 TGGGACATGGTCAGGAGTTTGTGGGAACAATGCATGCAGGAACCAATGCAGAAACCT 196  137 TGGGACATGGTCAGGAGTTTGTGGGAACAATGAACAATGCATGC	 srk of the	Query Match         61.6%; Score 176.2; DB 14; Length 421;           Best Local Similarity 83.8%; Pred. No. 1.6e-37;         Matches 212; Conservative 0; Mismatches 38; Indels 3; Gaps 1;           QY         20 AGTAATAGGTAAGTTTGCTACCATCATCTTCTTTTGCTGCTCTTTGTTCT 79           QY         1 ACTAGGTGATCATGGTAAGTTTGCTACCATCATTTTTTTT

Oy 257 CTTCCCATGTTAA 269

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Coarch Completed: May 18, 2004, 19-0

Search completed: May 18, 2004, 19:00:29 Job time: 2384.6 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	pti	AR014691 Sequence AR432391 Sequence AR432395 Sequence AR432389 Sequence	AR014686 Sequence AR432386 Sequence	BV010709 MASC STS1 BV010696 MASC STS1	BV010710 MASC STS1 BV010700 MASC STS1	AB017065 Arabidops	AC004747 Arabidops BV010699 MASC_STS1	BV010698 MASC STS1 BV010707 MASC STS1	BV010/11 MASC_SISI AX412406 Sequence	AX412601 Sequence AX651878 Sequence	AY060506 Arabidops A68645 Semience 13	X91916 A. Challana	AIUSZZ36 AIADIQODB BV010712 MASC STS1	BV010697 MASC SISI BV010667 MASC STS1	BV010673 MASC_STS1 RV010671 MASC_STS1	BV010670 MASC STS1	ACU07396 Genomic s AX412329 Sequence	AX412502 Sequence	AXS90057 Sequence	BD174927 Disease t	Aiiss/e/ Aiamiuops U18557 Raphanus sa	A68647 Sequence 15	A28873 K.Bacivus A A39549 Sequence 37	A63404 Sequence 19	AR130272 Sequence AR130272 Sequence R31545 Intihacteri		1 linear PAT 05-DEC-1998		. and Rosenberger, C.Annette. r controlling plant pathogenic	
SUMMARIES	ID	AR014691 AR432391 AR014689 AR432389	AR014686 AR432386		BV01071	AB017065	AC004747 BV01069		AX412406				BV01071	BV01069 BV01066		BV01067											270 bp DNA ent US 5773696. 145		l., Wu,Y.Shun nd methods fo	A 14 30-JUN-1998;
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Antifungal polypeptide and methods for controlling plant pathogenic
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Liang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.
Antifungal polypeptide AlyAFP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 12 25-NOV-2003;
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ilarity 100.0%; Pred. No. 3.8e-36;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.8e-36;
ive 0; Mismatches 0;
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                            Patent: US 5773696-A 12 30-JUN-1998;
Location/Qualifiers
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AR432389
AR432389.1 GI:40194666
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AR014686
AR014686.1 GI:3972140
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1. .286
/organism="unknown"
                                                                                /organism="unknown"
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1 (bases 1 to 286)
Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
                                                                                                                                                           1 AAGGITGIGCGAGAGCCAAGIGGGACATGGTCAGGAGITTGIGGGAACAACAATGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AAGTTGTGCGAGAGAGACCAAGTGGGAACATGGTCAGGAGTTTGTGGGAACAACAACAATGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 CAGGAACCAATGCAGAAACCTTGAAAGAGAGAACAAGGAACTTGGCAACTATGTCTTCCC
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknowu.
Unclassified.
I (bases 1 to 270)
Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
Antifungal polypeptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi
Patent: US 6653280-A 14 25-NOV-2003;
Location/Qualifiers
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                                                                                            Length 270;
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                            Ouery Match 100.0%; Score 154; DB 6; Best Local Similarity 100.0%; Pred. No. 3.8e-36; Matches 154; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                       121 AGCTCACAAAIGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                             228 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 261
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AR014689
AR014689.1 GI:3972143
             1. .270
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                   AR432391 270 bp 1
Sequence 14 from patent US 6653280.
AR432391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unknown"
/wol_type="genomic DNA"
location/Qualifiers
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Best Local Similarity 100.0
Matches 154; Conservative
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                source
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AR014689
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AR432391
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each 400 uM
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                Email: schmid@ice.mpg.de
         GI:32963207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
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Polymerization:
PCR Cycles:
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MEDLINE
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           1 (bases 1 to 500)
Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                     PAT 18-DEC-2003
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MASC_STS16442 Arabidopsis thaliana (Landsberg erecta accession)
genomic DNA Arabidopsis thaliana STS genomic, sequence tagged site.
BV010709
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Liang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.
Antifungal polypeptide AlyAPP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 9 25-NOV-2003;
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91.0%; Score 140.2; DB 6; Length 500;
Best Local Similarity 94.8%; Pred. No. 6.1e-32;
Matches 145; Conservative 0; Mismatches 8; Indels 0
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                                                                                                                                                         91.0%; Score 140.2; DB 6
94.8%; Pred. No. 6.1e-32;
1ve 0; Mismatches 8
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1. .500
/organism="unknown"
/mol_type="unassigned DNA"
                                                              Patent: US 5773696-A 9 30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9 from patent US 6653280. AR432386
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/mol_type="genomic DNA"
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Matches 145;
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Best Local &
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (Bases I to $26)
Schmid,K.J., Sorensen, T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weisshaar,B.
Large-Scale Identification and Analysis of Genome-Wide
Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
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Strain="Landsberg erecta"

(db xref="taxon:3702"

(clone lib="Azabidopsis thaliana (Landsberg erecta
accession) genomic DNA

Anote="Genomic DNA prepared from rosette leaves. DNA was
amplified and directly sequenced from both directions and
assembled into a consensus sequence. Note: Sequencing
granted in the context of the GABI Arabidopsis VerbundI.

Genetic Diversity, 'Bstablishment of high-efficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 degrees for 2.00 minute(s) 94 degrees for 0.50 minute(s) 58 degrees for 0.50 minute(s) 72 degrees for 1.00 minute(s) 35
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                                                                                                                                                                                                                                                                                                                                                                                                Synonyms: PCP16C2_ler.a
Contact: Karl Schmid
Department of Genetics and Evolution
Max-Planck-Institute of Chemical Ecolog
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer A: CGCTGCTCTTGTTCTCTTTG
Primer B: AAACAACCGTTGTTGGTCA
STS size: 526
PCR Profile:
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 575)
Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weisshaar,B.
Large-Scale Identification and Analysis of Genome-Wide
Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BV010710 575 bp DNA linear STS 18-JUL-2003
MASC_STS16443 Arabidopsis thaliana (Weiningen-0 accession) genomic
DNA Arabidopsis thaliana STS genomic, sequence tagged site.
                                                                                                                                                                                                                                                              486 AAGTIGIGCGAGAAGCCAAGIGGIACTIGGICAGGAGITIGCGGAAACAGCAAIGCAIGC 427
                                                                                                                                                                                                                                                                                                         62 AGGAACCAATGCAGAAACCTTGAAAGAGAGAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                           426 AAGAATCAGTGCATTAACCTTGAAGGAGCAAAACATGGATCTTGCAATGTCTTCCCA 367
                                                                                                                                                                                                                           61
                                                                                                                                                                                                                   Gaps
                   Thomas Altmann
                                                                                                                                                                             ;
0
                                                                                                                              DB 11; Length 574;
                                                                                                                       Query Match 79.6%; Score 122.6; DB 11; Length Best Local Similarity 87.6%; Pred. No. 1.4e-26; Matches 134; Conservative 0; Mismatches 19; Indels
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              genome-wide mutation detection, PIs: T
Thomas Mitchell-Olds, Bernd Weisshaar"
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Polymerization: 72 degrees for 1.00 minui
PCR (cycles: 35
Thermal Cycler: Perkin Elmer Geneamp9600
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Contact: Karl Schmid
Department of Genetics and Evolution
Max-Planck-Institute of Chemical Ecology
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: +49-3641-571465
Fax: +49-3641-571405
Fax: +49-3641-571405
Fax: +49-3641-571405
Fax: +A3-3641-571405
Fax: +A3-3641-571405
Fax: +A3-3641-571405
Fax: +A3-3641-571405
Fax: +A3-3641-571405
Fax: +A3-3641-575
FCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                 122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                         366 GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 334
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Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
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each 400 uM
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BV010710.1 GI:32963208
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MgCl2: 1
KCl: 5
Tris-HCl: 1
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PUBMED
COMMENT
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BV010710
LOCUS
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KEYWORDS
SOURCE
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicacae; Arabidopsis.

(bases 1 to 574)
Schmid, K.J., Sorensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
Mitchell-Olds, T., and Weisshaar, B.
Large-Scale Identification and Analysis of Genome-Wide
Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
22683290
                                                                                                                                                                                                                               BV010696 574 bp DNA linear STS 18-JUL-2003 MASC STS16441 Arabidopsis thaliana (Eifel-2 accession) genomic DNA Arabidopsis thaliana STS genomic, sequence tagged site.
Jobbes "Genomic DNA prepared from rosette leaves. DNA was amplified and directly sequenced from both directions and sassembled into a consensus sequence. Note: Sequencing granted in the context of the GABI Arabidopsis VerbundI: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for
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/clone_lib="Arabidopsis thaliana (Eifel-2 accession)
genomic_DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Presoak: 94 degrees for 2.00 minute(s)
Denaturation: 94 degrees for 0.50 minute(s)
Annealing: 58 degrees for 0.50 minute(s)
POlymerization: 72 degrees for 1.00 minute(s)
PCR Cycles: 35
Thermal Cycler: Perkin Elmer Geneamp9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synonyms: PCP16C2_ei2.a
Contact: Karl Schmid
Department of Generics and Evolution
Max-Planck-Institute of Chemical Ecology
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571465
Fax: + 49-3641-571465
Email: schmid@ice.mpg.de
Primer A: CGCTGCTCTTGTTCTCTTTG
STimer B: AAACAAACCGTTGTTGGTCA
STS size: 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .574
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Eifel-2"
                                                                     122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                 162 GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 194
                                                                                                                                                                                                                                                                                                                                                  STS.
Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Template: 20 - 100 ng
Primer: each 1 uM
dNTPS: each 400 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul
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Location/Qualifiers
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BV010696.1 GI:32963194
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KCl: 50 mM
Tris-HCl: 10 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protocol:
Template:
Primer:
dNTP8:
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MgC12:
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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BV010696/c
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MEDLINE
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602 bp
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Contact: Karl Schmid
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BV010703.1 GI:32963201
                                                                                                                                                                                                          rgC12: 1.5 mM
KC1: 50 mM
Tris-HC1: 10 mM
pH:
               PCR Cycles:
                                                    Protocol:
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PUBMED
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Large-Scale Identification and Analysis of Genome-Wide
Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BV010700 578 bp DNA linear STS 18-JUL-2003 MASC_STS16437 Arabidopsis thaliana (Lezoux/Puy-de-Dome-0 accession) genomic DNA Arabidopsis thaliana STS genomic, sequence tagged site.
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                                                                                                                                                                       Juote="Genomic DNA prepared from rosette leaves. DNA was amplified and directly sequenced from both directions and sessembled into a consensus sequence. Note: Sequencing granted in the context of the GABI Arabidopsis VerbundI: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PIS: Thomas Altmann, Thomas Mitchell-Olds, Bernd Weisshaar"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.

1 (bases 1 to 578)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 AAGTIGIGGAGAAGCCAAGIGGIACTIGGICAGGAGITITGCGGAAACAGCAAIGCAIGC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 AAGAATCAGTGCATTAACCTTGAAGGAGCAAAACATGGATCTTGCAACTATGTCTTCCCA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                 /db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana (Weiningen-0 accession)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AGGITGIGCGAGAGACCAAGIGGACAIGGICAGGAGITTGIGGGAACAACAAIGCAIGC
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s for 0.50 minute(s)
s for 0.50 minute(s)
s for 1.00 minute(s)
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Contact: Karl Schmid
Department of Genetics and Evolution
Max-Planck-Institute of Chemical Ecology
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571465
Fax: + 49-3641-57402
Fax: + 49-3641-57402
Frax: + 60-3641-57402
Primer A: CGCTGCTCTTGTCTTTG
Primer B: AAACAAACGTTGTTGGTCA
                                                    organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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                                                                     type="genomic DNA"
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94 degrees 1
58 degrees 1
72 degrees 1
                                                                                         /strain="Weiningen-0"
Location/Qualifiers
1. .575
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                                                                                                                                                          genomic DNA"
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Annealing:
Polymerization: 7
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PCR Profile:
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1 (bases 1 to 602).
Schmid, K.J., Sorensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
Mitchell-Olds, T. and Weisshaar, B.
Large-Scale Identification and Analysis of Genome-Wide
Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; euroside II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana (Lezoux/Puy-de-Dome-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AGGAACCAATGCAGAACCTTGAAAGAGCAGAACAGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AGGITGTGCGAGAGACCAAGTGGACAIGGTCAGGAGTTTGTGGGAACAACAATGCATGC
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Thermal Cycler: Perkin Elmer Geneamp9600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Lezoux/Puy-de-Dome-0"
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79.6%; Score 122.6; DB 1.
Best Local Similarity 87.6%; Pred. No. 1.4e-26;
Matches 134; Conservative 0; Mismatches 19
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                          .c.wpiate: 20 - 100 ng
Primer: each 1 uM
dNTPs: each 400 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
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ó

Tracheophyta;

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Direct Submission Makamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Risarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:61-438-52-3935, Fax:81-438-52-3934)

Address for correspondence: kaos@kazusa.or.jp

Rot the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd graph.cgi?c=MFCi6 Genes with similarity to proteins in the databases are described in 'protein' or 'nofe' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, Http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), MRtGenez (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SpliceBredictor (Volker Brendel, Staniford University, Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).

This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The S' clone is K15C21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INEDDSRIIHTSKOPSYFSIINSSIQNPRFFVLETPKPVSIITPVQATDVQSTIKCAR
LHGIHIRTRSGGHDYEGLSYMAKSRPFVVIDLRNLRSITLDVDNRTGWVQSGATIGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MEILRFLLSLFIYFLLLNLSLSHFPSISAQRTNHENFLKCLSHR
                                                                                                  Taneko, T., Katoh, T., Sato, S., Nakamura, Y., Asamizu, E., Kotani, H., Miyajima, N. and Tabata, S.
Structural analysis of Arabidopsis thaliana chromosome 5. IX.
Squence features of the regions of 1,011,550 bp covered by seventeen Pl and TAC clones
DNA Res. 6 (3), 183-195 (1999)
                    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/product="berberine bridge enzyme-like protein"
/protein_id="BAB09147.1"
/db_xref="GI:9758693"
Bukaryota, Viridiplantae, Streptophyta, Embryophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="berberine bridge enzyme"
/note="CDS is reported in Acc# AB011475
gene_id:X9L2.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
complement(1020. .1516)
/product="berberine bridge enzyme"
/note="CDS is reported in Acc# AB011475
gene_id:K9L2.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'organism="Arabidopsis thaliana"
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complement(4691. .6298)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="MFC16"
/clone_lib="Mitsui P1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1. .926)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon start=1
                                                                                                                                                                                                                                                                                                                                 (bases 1 to 61290)
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                                                                                                                                                                                                                                                                                                    10470850
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                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                REFERENCE
                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                         PUBMED
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                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Juctes Genomic DNA prepared from rosette leaves. DNA was amplified and directly sequenced from both directions and sasembled into a consensus sequence. Notes Sequencing gratted in the context of the GABI Arabidopsis Verbundl: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PIS: Thomas Altmann, Thomas Mitchell-Odds, Bernd Weisshaar:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:3702"
/clone lib="Arabidopsis thaliana (Gueckingen-0 accession)
genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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0
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                                                                                                                                                                                                                                                                          94 degrees for 2.00 minute(s) 94 degrees for 0.50 minute(s) 58 degrees for 0.50 minute(s) 72 degrees for 1.00 minute(s)
                                                                                                                                                                                                                                                                                                                                      Annealing: 58 degrees for 0.50 minut
Polymerization: 72 degrees for 1.00 minut
PCR Cycles: 35
Thermal Cycler: Perkin Elmer Geneamp9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .602
/organism="Arabidopsis thaliana"
                    Max-Planck-Institute of Chemical Ecology
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571465
Fax: + 49-3641-571402
Email: schmid@ice.mpg.de
Primer A: CGCTGCTCTTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 357
  Department of Genetics and Evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Template: 20 - 100 ng
Primer: each 1 uM
dNTPs: each 400 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/strain="Gueckingen-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB017065.1 GI:3510341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COL: 1.5 mM KCl: 50 mM Tris-HCl: 10 mM PH:
                                                                                                                                                                                                                                                                                                         Denaturation:
                                                                                                                                                                                                                        STS size: 602
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protocol:
Template:
                                                                                                                                                                                                                                                                                  Presoak:
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MgC12:
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source

FEATURES

STS ORIGIN

Š g ò g ò YYEIGKLSKSLAFPAGLYPTVGIGGQFGGGGGYGTLMRKYGLSADNVIDAHIVDANGSF LDRQCMGEDFFWAIRGGGGSSFSVVLSWKIRLLDVPSVVTVFKVVKTSEKEAVSIINK WQYIADKVPNDLFIRAMLQKETEVYASFPGLYLGPVSDLLALMKOKFPELGLEIGNCR

Arabidopsis thaliana (thale cress) Arabidopsis thaliana

ORGANISM

RESULT 12 AB017065/c LOCUS

DEFINITION ACCESSION VERSION KEYWORDS

CDS

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join(34960. .35217,35310 .35423,35504. .35611,35705. .35796,
35890. .36031,36106. .36200,36301. .36430,36509. .36653,
36662. .37088)
/note="contains similarity to UDP-glucose 4-epimerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22689 AAGTIGIGGGAGAAGCGAAGIGGACAIGGICAGGCGITIGCGGAAACAGTAAIGCAIGC 22630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22629 AAGAATCAGTGCATTAACCTTGAGGGAGCAAAACATGGATCTTGCAACTATGTCTTCCCA 22570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
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/product="calmodulin-like protein"
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HDGRVDFFFKNMMQTVVVPS"
join (32184. 32265, 32365. 32609)
/note="gb] AAF30348.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC004747 87080 bp DNA linear PLN 11-MAR-2002
Arabidopsis thaliana chromosome 2 clone T19L18 map B68, complete
sequence.
AC004747
HTG.
                                                                                                                                                                                                                                                                             /trānslation="MMREEIGEGDETKKTQMYRDGVSYWEGVBASVDGVLGGYGHVND
BADIGSBEVEKTLLGRELWNVGAAQHLVALDGSGIGRITYKLLIRYKHEVDELEPY
AQFLDAARBNLASAGSTHKATNFFVVPLOBFTPAAGRYDVJWVQWCIGHLDVDFVVS
FFNRAKDLFWIKKILASPDRIHTSNSSFANVGYISIEQRNLQSFLQWHNFQDQKGLPQ
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/translation="WIEVTRANDTREWIENIATSEOGTSGSGLGWIIRNSHGT"
FMECGMSKRQGRAPVEESECTALIWALQSSWNLGYIKIEFDGDNLSIIRLINGKAVNP
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/db_xref="GI:9789701"
/translation="MLNSSGVRTQRRSPRPLSLGGRKIITPTKFAYDHHNPDKVLDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMDCLEPKTKNNLTGKLLLVASLL1LAIIVISQSSSFTSPSAFSQREEGVTHVLVTGG
                            complement(join(27805. .27967,28028. .28125,28368. .28469,28564. .28674,28765. .28823,28902. .29049,29157. .29234))
//note="gene_id:MFC16.11
unknown proTein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 61290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.6%; Score 122.6; DB 8;
llarity 87.6%; Pred. No. 1.4e-26;
Conservative 0; Mismatches 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene_id:MFC16.13
similar to unknown protein"
                                                                                                                                                                                        experimental
         RVKTRVDPTDFFCDEQSIPLVNKVT'
                                                                                                                                                                                                                 /protein_id="BAB09152.1"
/db_xref="GI:9758698"
                                                                                                                                                                                                                                                                                                                                                                                                                                  30731. .31276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         id:MFC16.15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon start=1
                                                                                                                                                                                        /evidence=not
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Matches 134; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122
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AC004747/c
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HVRTRSAGHCYEGLSYLAYNKPRAVLDLRNIRSISTSDVDNRTGWVQTGATAGELYYEI
GKTTKSLAFBAGHPPTVGVGGOFSGGSYGTLLRKYGLAADNIIDALVVDASGRILDRO
AMGEDYFWA.IRGAGGSSFGVILSWKYALVDVBSTITVPKVQKTSKKRAVRIIKKWQYA
ADKVPDDLFIRTTLERSNKNAVHALFTGLYIGPVNNLLALMEEKFPELGLEKEGCEEN
SWIESVLUMAFDFPKGEBLGYTINRERTSLFKKGNDFVQDF IPBAALGEINRRLEAPE
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VDSVYEFMIPPVSKSPRGAYUNFKDMDLGWYLGKKKTKYEEGKSWGVKYFKNNFERLV
EMSWIESVLWFIKGESMEILAKRKRTSRSFKGKDDFIEEPIPKTAIQYLWRRFEAPEA RLAKIILTFPGGKMSEIADNEIPFPHREGNLYEIQYLAYWSEBEDKNKTNTEKYLRWV ESYVERWIPYVSKSPRRAYNYRRDIDLGMYLGLNMKTKYEEAKVWGVKYFKNNFDRLV RVKTNVDPMPFFCDEQSIPIMKYVNDI '9791'. 7708,7913'. .8716,8797'. .8955,9026'. .9446',9636'. '9820')
/note="contains similarity to En/Spm-like transposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MAKSATIITFLFAALVLFAAFEAPTMVEAQKLCEKPSGTWSGVC
GNSNACKNQCINLEGAKHGSCNYVFPAHKCICYVPC"
complement (24139. .25740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVEEKLEEFKSEKSTRALKLALILFLAKVWRADSKGBSKIEBFLLEITONVRACETFP
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ACCESSION VERSION KEYWORDS

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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
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1 (bases I to 87080)
Rounsley,S.D., Kaul,S., Lin,K., Ketchum,K.A., Crosby,M.L.,
Brandon,R.C., Sykes,S.M., Mason,T.M., Kerlavage,A.R., Adams,M.D.,
Somerville,C.R. and Venter,J.C.
                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 87080)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712
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Direct Submission
Submitted (27-FB2-2002) The Institute for Genomic Research, 9
Submitted (27-FB2-2002) The Institute for Genomic Research, 9
Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
On Apr 18, 2002 this sequence version replaced gi:6598441.

1. .87080
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          SOURCE
ORGANISM
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REFERENCE
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                                                                                                                                                           AUTHORS
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEDLKVSIHDPTITLLEVELIALKSGLNQAVSLGINHISICCDHEYIFELVMGISTPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SALSEYIKALVKVDRLDQSELVRTLQRGIAGVAREEETFGGLGAFRNVGKPTKDGVLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (join(13028. .13137,13438. .13642,13658. .13791,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(9239. .9395,9823. .9910,9992. .10264,10403. .10639,
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           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
1 (Basse It o 580)
Schmid; K.J., Sorensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
Mitchell-Olds, T. and Weisshaar, B.
Large-Scale Identification and Analysis of Genome-Wide
Genome Res. 13 (6), 1250-1257 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGITTGIGGGAACAACAAGATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 degrees for 2.00 minute(s) 94 degrees for 0.50 minute(s) 58 degrees for 0.50 minute(s) 72 degrees for 1.00 minute(s) 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermal Cycler: Perkin Elmer Geneamp9600
                                                                                                                                                                                                                                                                                                                                                                                                     Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571465
Fax: + 49-3641-571402
Email: schmidaice.mpg.de
Primer A: CGCTGCTCTTGTTCTTTG
Primer B: AAACAAACCGTTGTTGGTCA
STS size: 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                Synonyms: PCP16C2 cvi0.a
Contact: Karl Schmid
Department of Genetics and Evolution
Max-Planck Institute of Chemical Ecology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tag Polymerase: 0.05 units/ul
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each 1 uM
each 400 uM
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Location/Qualifiers
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KCl: 50 mM
Tria-HCl: 10 mM
pH: 8.3.
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PCR Cycles:
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nes 133; Conserv
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Matches
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PUBMED
COMMENT
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISVVCRKKLQVDMEEBGTLVRADNIKHAGTPSPSKFSPYSLYFKGLMKGPIHDSAITI
LEBELMALKYGLSBAVTLGINHISICCDNNOIFBWWGRSTPQBENIAMLIBDVQGIR
KQFTSSIAVLVTRNQVEFRYKVAMBAICFRTKIAFSVSSDVPALFHPKKTCTICFDDD
INADMMFYIQQCGHNFCSBCVKRHIEGSLITCPSYRCKSKLTYGSCVNILTPKVKEMM
IQRNGEDSIPYDDRYZCPNPTCSALMSVTELDQLTGNVDMSFAMDVELMLDVALLWYMY
RIFQLNVSSQKSKH"
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MASC_STS1643B Arabidopsis thaliana (Cap Verde Islands-0 accession)
genomic DNA Arabidopsis thaliana STS genomic, sequence tagged site.
BV010699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānglation="WINGGGGMSSGEGFRRRSSGEGFPAREFRWWVSGDRVFPRGFFG
EGVQVGVPTVVSGEGVPAKVPGGDFSGKKVPAVVFRRVSSSDGGGRGSGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tränglation="MCFYLLSEKNQTHPSPSSSPFLSEQRTQPKQKSMLDMSESVLTA
MYSWFTPTVLFVFLNLMIGTIAISSSFSSKSNDPNQTQIQRSPSMIHRLKSINFSSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
  PFCVKCKVSWHNNLSCDEYKTLHPNPTENDGRLRDLANBKSWRQCSKCKHMI ELSSGC
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                                                                                                                                                                                                                                                                                                                                   //octe="wynonym: T191.18.7; predicted by genefinder"
complement(join(<20678. .20845,20919. .>21065))
/gene="At.2926120"
complement(join(20678. .20845,20919. .21065))
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/gene="At.2926120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8; Length 87080;
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Pred. No. 1.3e-26;
0; Mismatches 19; Indels
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/protein_id="AAC31225.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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complement(21381..21433)
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complement(21881..21943)
/rpt_family="AT_rich"
complement(22821..23626)
/gene="At226110"
/note="Stronyw::T19118.8"
complement(<22621..>23626)
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complement (18680. .18732)
/rpt family="AT_rich"
19418. .19445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (22697, .23626)
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complement(20678. .21065)
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/rpt_family="(TGG)n"
21200. .21221
/rpt_family="(A)n"
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Best Local Similarity 87.6
Matches 134; Conservative
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Search completed: May 18, 2004, 17:59:04 Job time: 758.05 secs
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Large-Scale Identification and Analysis of Genome-Wide
Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
                                                                                                                                                                                            BV010698 STS16439 Arabidopsis thaliana (Konchezero accession) genomic DNA Ārabidopsis thaliana STS genomic, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Junce Genomic DNA prepared from rosette leaves. DNA was amplified and directly sequenced from both directions and assembled into a consensus sequence. Note: Sequencing granted in the context of the GABI Arabidopsis VerbundI: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PIS: Thomas Altmann,
                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids; eurosids II, Brassicales; Brassicaceae; Arabidopsis.
153 AAGAATCAGTGCATTAACCTTGAGGGAGCAAAACATGGATCTTGCAACTATGTCTTCCCA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .582
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Konchezero"
/db_xref="teaxon:3702"
/clone_lib="Arabidopsis thaliana (Konchezero accession)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 degrees for 2.00 minute(s) 94 degrees for 0.50 minute(s) 58 degrees for 0.50 minute(s) 72 degrees for 1.00 minute(s) 35
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PCR Cycles: 35
Thermal Cycler: Perkin Elmer Geneamp9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synonyms: PCP16C2_cs22491.a
Contact: Karl Schmid
Department of Genetics and Evolution
Max-Planck-Institute of Chemical Ecology
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571462
                                                                     213 GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 245
                                               GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.05 units/ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: schmid@ice.mpg.de
Primer A: CGCTGCTCTTGTTTG
Primer B: AAACAAACCGTTGTTGGTCA
STS size: 582
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 - 100 ng
each 1 uM
each 400 uM
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Tris-HCl: 10 mM
pH: 8.3.
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Annealing:
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Template:
Primer:
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MgCl2:
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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MEDLINE
PUBMED
COMMENT
                                                                                                                                                      RESULT 15
BV010698
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94 AAGTIGIGGAGAAGCCAAGIGGIACTIGGICAGGAGITIGCGGAAACAGCAAIGCAIGC 153
                                                                                                                                                                                                                                                                                                                                                               154 AAGAATCAGTGCATTAACCTTGAGGGAAAACATGGATCTTGCAACTATGTCTTCCCA 213
                                                                                                                                                                                                                                                                                                                                    62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                         2 AGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGTITGIGGGAACAACAAIGCAIGC
                                                                                                                                                                     Gaps
                                                                                                                                                                     .;
0
                                                                                                                 Length 582;
                                                                                                              Score 121, DB 11; Length 5
Pred. No. 4.3e-26;
0; Mismatches 20; Indels
Thomas Mitchell-Olds, Bernd Weisshaar"
<1. .>582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                 Query Match 78.6%;
Best Local Similarity 86.9%;
Matches 133; Conservative
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Aat44582 Amplified
Aat94584 Alyssum s
Aat9289 Alyssum s
Aat4581 Composite
Ad51221 Brassica
Ad651229 Brassica
Ad66378 Arabidops
Aav10632 A. thalia
Ab48680 Masabia j
Ab24241 Arabidops
Ab242436 Arabidops
Aav10633 A. thalia
Ab438650 Rs-AFP1 C
Aa438650 Rs-AFP1 C
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Aaz39123 Wasabia j
Abg28291 Wasabia j
Aaz39124 Wasabia j
Aav10646 A. thalia
Aat94577 Cloned 5'
Aag4577 Cloned 5'
Aag70130 Antimicro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raphanus
                                                                 May 18, 2004, 16:12:26 ; Search time 150.15 Seconds (without alignments) 4357.126 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                   1 aaggttgtgcgagagaccaa......tttgttacttcccatgttaa 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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Aaq70128 A
Aat72333 R
Aat68696 R
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                        3373863 seqs, 2124099041 residues
                                                                                                             US-10-681-972-12_COPY_116_269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             - nucleic search, using sw model
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AAT9289
AAT9289
AAT9481
ADC51221
ADC51223
ADA68378
AAV10632
ABZ14241
ABZ14241
ABZ42136
AAC918650
AAC70128
AAC70128
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AAZ39124
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geneseqn2001as:*
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L: genesequ1980s:*
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                                                                                                                                                                                                                                     seq length: 0 seq length: 2000000000
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RESULT 1  AAT94582  XX  AAT94582;  XX  AAT94582;  XX  AT94582;  XX  AT94582;  XX  Amplified Alyssum species antifungal polypeptide gene from pWON22652.  XX  Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;  XX  Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;  XX  Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;  XX  Alyssum sp.  XX  Alyssum sp.  XX  Alyssum sp.  XX  Alyssum sp.  XX  Alyssum sp.  XX  Alyssum sp.  XX  Alyssum sp.  XX  Alyssum sp.  XX  Alyssum sp.  XX  XX  XX  XX  XX  XX  XX  XX  XX
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the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum. The AlystP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic
                                                                                                                                                                                                                                                                        61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 120
                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                 1 AAGGITGIGGAGAGACCAAGIGGACAIGGICAGGAGTITGIGGGAACAACAAIGCAIG
                                                                                                                                                                                                          Gaps
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                                                                                                                                                             Query Match
100.0%; Score 154; DB 2; Length 270;
Best Local Similarity 100.0%; Pred. No. 1.9e-42;
Matches 154; Conservative 0; Mismatches 0; Indels 0
                                                                                                                        Sequence 270 BP; 75 A; 58 C; 60 G; 75 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                              AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                       228 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 261
                                                                                                                                                                                                                                                                                                                                                                         168
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AAT94574 standard; cDNA; 286 RESULT 2 AAT94574 

AAT94574;

(first entry) 12-MAY-1998 Alyssum species anti-fungal polypeptide AlyAFP cDNA sequence.

Antifungal polypeptide; AlyAFP; inhibition; transgenic plant; phytopathogenic fungus; resistance; ss.

location/Qualifiers 117. .269 /\*tag= a

product= "mature AlyAFP protein"
/note= "no start codon given at 5' end of sequence"

WO9737024-A2

09-0CT-1997

97WO-US005709. 27-MAR-1997; 96US-00627706 29-MAR-1996;

(MONS ) MONSANTO CO

Rosenberger CA;

Wu Υ,

Liang J, Shah D,

WPI; 1997-503109/46. P-PSDB; AAW35558.

Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi Claim 12; Page 68; 92pp; English.

This sequence encodes the mature protein of an antifungal polypeptide (AlyARP) isolated from plants of the genus Alyssum. The sequence was PCR amplified using primers AAT94583-T94584, and the resultant 264 bp fragment was cloned as a Bamil fragment into the expression vector pMOM32317 to generate plasmid pMOM32552. The AlyARP sequence in this plasmid is placed under control of an B35S promoter and the maize HSP70 intron I sequence. The protein can be used to control phytopathogenic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the cDNA sequence which encodes the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum. The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
                                                                                                                                                                                         CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 235
fungi, whilst the DNA can be used to produce transgenic plants that express the protein making them resistant to the phytopathogenic fungi
                                                                                                                                         116 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG
                                                                                                                                                                 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC
                                                                                                                 1 AAGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGITTGIGGGAACAACAAIGCAIG
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi.
                                                                                      0
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                                                               DB 2; Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "AlyAFP antifungal polypeptide"
                                                                                       0; Indels
                                     Sequence 286 BP; 80 A; 62 C; 65 G; 79 T; 0 U; 0 Other;
                                                                                                                                                                                                                                  AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 269
                                                             100.0%; Score 154; DB 2;
100.0%; Pred. No. 2e-42;
ive 0; Mismatches (
                                                                                                                                                                                                                    AGCTCACAAATGTATTTGTTACTTCCCATGTTAA
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                                                                                                                                                                                                                                                                                                                                                                                       Alyssum species AlyAFP cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
53. .292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Fig 1; 92pp; English.
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439.
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                                                                                       154; Conservative
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                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shah D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW35560
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                                                                                                                                                                                         176
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                                                               Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
219 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACAGGATCTTGCAAACTATGTCTTCCCA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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/product= "Brassica oleracea defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                                      composite disease resistance; pathogenic bacteria; rice white leaf blight, brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                         Brassica oleracea defensin protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                  antimicrobial protein; defensin; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.6%; Score 122.6; DB 9; 87.6%; Pred. No. 1.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
                                                                                      GCTCACAAATGTATTTGTTACTTCCCATGTTAA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                 122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA
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1. .243
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; SEQ ID NO 1; 34pp; Japanese.
                                                                                                                                                                                                                  BP
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Matches 134; Conservative
                                                                                                                                                                                                                ADC51221 standard; DNA; 394
                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica oleracea.
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                                                                                                        279
                                                                                                                                                                                                                                                         ADC51221;
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                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                     %XCZCCCCCCCXXXX1112XBXX11X11XBXBX11111X8XX4X4X8XXBX11X1X8XXX
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                       윤
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                                                                                                                                                                                        139 AAGGTIGIGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGGAACAACAATGCATG 198
                                                                                                                                                                                                                                   CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                   09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the cDNA sequence encoding the antifungal polygeptide AlyAFP, from plants of the genus AlySesum. The sequence represents a composite of the sequences isolated by 5' and 3' RACE (Rapic Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The AMPAFP PolyPeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
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                                                                                                                                                                                                                                                             CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAAACAGGATCTTGCAACTATGTCTTCCC
                                                                                                                                                   1 AAGGTTGTGCGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide; AlyAFP; inhibition; transgenic plant; penic fungus; resistance; ss.
                                                              Length 481;
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                                                                                                        0; Indels
                          Sequence 481 BP; 147 A; 88 C; 91 G; 154 T; 0 U; 1 Other;
                                                 Best Local Similarity 100.0%; Score 154; DB 2; Best Local Similarity 100.0%; Pred. No. 2.4e-42; Matches 154; Conservative 0; Mismarches
                                                                                                                                                                                                                                                                                                                      121 AGCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                             AGCTCACAAATGTATTTGTTACTTCCCATGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenberger CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 67; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MONS ) MONSANTO CO.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phytopathogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antifungal
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Matches
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Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression
                                                                                                                                                                                                                                                                                                                             Chang H, Ch
Katagiri F,
                                                                                                          20-NOV-2003
                                                                                                                                                                                                                                 03-JAN-2003
                                                                                 ADA68378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                 RESULT 7
                                                ADA68378
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                                                                                  임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to disease caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                            antimicrobial protein; defensin; transgenic plant; composite disease resistance; pathogenic bacteria; rice white leaf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 79.6%; Score 122.6; DB 9; Length 426; Best Local Similarity 87.6%; Pred. No. 1.3e-31; Matches 134; Conservative 0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "Brassica defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                    (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
               211 GCTCACAAGTGTATTTGCTACTTCCCTTGTTAA
                                                                                                                                                        Brassica defensin protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; SEQ ID NO 3; 34pp; Japanese.
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-2001; 2001JP-00283117
                                                                                                                                                                                                                                                                                                                                                                                                             18-SEP-2001; 2001JP-00283117
                                                                                 ADC51223 standard; DNA; 426
                                                                                                                                (first entry)
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P-PSDB; ADC51224.
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                                                                                                                                18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003.
                                                                                                                                                                                                                                                      Brassica sp
                                                                                                         ADC51223;
                                                                     ADC51223
                                                          RESULT
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The present invention relates to a method (M1) for identifying genee involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 AAGTTGTGCGAGAGGCCAAGTGGGACATGGTCCGGAGTTTGCGGAAACAGTAACGCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; bacterial infection; fungal infection; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xon (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SA, Hor
Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.5%; Score 119.4; DB 7; Length Best Local Similarity 86.3%; Pred. No. 1.3e-30; Matches 132; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 243 BP; 58 A; 56 C; 59 G; 70 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glazebrook J, Goff
Whitham S, Xie Z,
211 GCTCACAAGTGTATTTGCTACTTCCCTTGTTAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCACAAAIGTATCTGCTACTTCCCAIGTTAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCACAAATGTATTTGTTACTTCCCATGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; SEQ ID NO 747; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana gene, SEQ ID 747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-2001; 2001WO-IB001105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cooper B, S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
AAV10632
ID AAV10632 standard; DNA; 403
                                                                                                                                                                                          ADA68378 standard; DNA; 243
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quan S,
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P-PSDB; ABP53725
                                                                                        Eutrema wasabi,
                                                                                                                                                      JP2002272292-A.
                           02-JAN-2003
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                                                                                                                                                                       24-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ14241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
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                                                                                                                                                                                                                                                                                                                                           Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes the Arabidopsis PDF1.1 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                        Manners JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                            Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.5%; Score 119.4; DB 2; Length 403; 86.3%; Pred. No. 1.5e-30;
                                                                                                                                                                                                                                                                                        Terras FRG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 GCTCACAATGTATCTGCTACTTCCCATGTTAA 268
                                                                                                                                                                                                                                                                                      Thomma BPHJ, Penninckx IAMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                             /*tag= c
/product= "PDF1.1"
/note= "plant defensin"
                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 1, 72pp, English.
                                                                                                                                                                                                                                   97WO-GB001672.
                                                                                                                                                                                                                                                    96GB-00013753
                                                                                                                 26. .268
/*tag= a
26. .113
                         (first entry)
                                                                                                                                                    .265
                                                                                                                                           *tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 86.3
hes 132; Conservative

 A. thaliana PDF1.1 DNA

                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                  WPI; 1998-086663/08.
                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW40345.
                                                                                                                                                                                                                                                                     (ZENE ) ZENECA
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                                                                                                                                                                                               WO9800023-A2
                                                                                                                                                                                                                                   20-JUN-1997;
                                                                                                                                                                                                                                                    01-JUL-1996;
                         23-JUN-1998
                                                                                                                                   sig_peptide
                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                 08-JAN-1998
                                                                     fungi; ss
        AAV10632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                  Kazan K;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
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ABQ82690 ID ABQ82690 standard; cDNA; 243 BP.

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210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                  Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 AAGTTGTGCGAGAAGTCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAACAACAATGCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a disease-resistant plant in which wasabi gamma-thionin gene is introduced. Also described is a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.5%; Score 117.8; DB 6; Length 243; Best Local Similarity 85.6%; Pred. No. 4.4e-30; Matches 131; Conservative 0; Mismatches 22; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A disease-resistant plant in which wasabi gamma-thionin gene introduced, creation of the disease-resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana stress regulated gene SEQ ID NO 2046.
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                                                    Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 243 BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 TATCACAGAIGTATCTGTTACTTCCCAIGTTAA 243
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                                                                                                                                                                                                                                                                                          /*tag= a
/product= "gamma-thionin"
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 8; 11pp; Japanese.
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(first entry)
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Zhu T;

Wang X,

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cell has been exposed, comprising: (a) contacting nucleic acid arrepresentative of expressed polymucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polymucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants. Cells and seeds and in producing plants with increased tolerance to abictic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to berwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Posttranscriptional gene silencing; PTGS; plant; transformation; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 144; SEQ ID NO 2046; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                  24-AUG-2000; 2000US-0227866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                                                                                                                          24-AUG-2001; 2001WO-US026685.
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Best Local Similarity 85.6%;
Matches 131; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kreps J,
Arabidopsis thaliana
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                                                                   WO200216655-A2
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                                                                                                                                           28-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ42136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
ABZ42136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE SEA TO A SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF TH
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Location/Qualifiers 1. .243

ВP

(first entry)

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The invention relates to a novel isolated polynucleic acid segment modulated within a cell by posttranscriptional gene silencing (PTGS). The invention specifically relates to a method to identify an expression product that is modulated by PTGS. The polynucleotide is useful for modulating the gene expression within a cell by PTGS, by introducing the polynucleic acid into a cell and expressing the nucleic acid segment in the cell to form a product. The polynucleic acid segment is also useful for augmenting a cell and expressing the nucleic acid segment contacting a plant cell with the segment to produce a transformed plant cell, and growing the transformed plant to produce a transformed plant segments of A. thaliana cDNA modulated by PTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AAGAATCAGTGCATTAACCTTGAAGGAGCCAAACATGGATCATGCAACTATGTCTTCCCA 210
                                                                                                                                                                                                                                                                                 Novel polynucleic acid segment useful for modulating gene expression within a cell by posttranscriptional gene silencing, and for augmenting plant cell genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGAACCAATGCAGAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGITIGIGGGAACAACAAIGCAIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7; Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 117.8; DB 7; Length Pred. No. 4.4e-30; 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCACACAAGTGTATCTGTTACGTCCCATGTTAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                          Chang
                                                                                                                                                                                                                                                                                                                                                       Claim 18; Page 425-426; 438pp; English.
                                                                                                                                                                                                            Wang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 32. .274
                                                                                                                                                           (SYGN ) SYNGENTA PARTICIPATIONS AG. (FRIE-) FRIEDRICH MIESCHER INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                          Glazov EA, Meins F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.6%;
Matches 131; Conservative (
                                                                                           05-APR-2002; 2002WO-EP003806
                                                                                                                           06-APR-2001; 2001US-0282049P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV10633 standard; DNA; 400
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDF1.2 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                         WPI; 2003-103337/09.
P-PSDB; ABP81292.
                              WO200281695-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. thaliana
                                                            17-0CT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fungi; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1:
AAV10633
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                                                                                                                                                                                                                                                                                                                                                                                     invention relates to identifying a stress condition to which a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
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This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA ilbrary. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product, which was further reamplified with the same primers and digoxigenin-11-dUTP instead of dTTP to give a digoxigenin-11-dUTP instead of dTTP to give a digoxigenin-11-dUTP instead of dTTP to give a digoxigenin-11-dUTP instead of dTTP to give a digoxigenin-11-dUTP instead of dTTP to give a digoxigenin-11-dUTP instead of dTTP to give a digoxigenin-11-dUTP instead of dTTP to give a digoxigenin-11-dUTP instead of dTTP to give a digoxigenin-12-dUTP instead of dTTP to give a digoxigenin-13-dUTP instead to screen a lambda ZAPII CDNA library by in situ product, the pBluescript phagemid form with the aid of helper phage additional screening rounds with the same probe. Inserts were excised in their size compared by agarcose gel electrophoresis. Four clones had inserts size of approx. 400bp the others between 250-300bp. The inserts of the length of their 5' and 3' UTR's. The longest sequence is given here. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                              of plants - e.g. brassica or resistance to fungal and bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 414;
                                                                                                                                                                                                                                                                                                                                                       Terras FRG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                     Rees SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.5%; Score 117.8; DB 2
85.6%; Pred. No. 5.5e-30;
tive 0; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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                                                                                                                                                                                                                                                                                                                                                       Cammue BPA, Osborn RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biocidal proteins isolated from seeds dahlia, useful for increasing plants'
Location/Qualifiers
16. .256
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 21; Fig 35; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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92GB-00003038.
92GB-00013526.
                                                                                                                                                                                                                                                                                                            ICIL ) IMPERIAL CHEM IND PLC.
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                                                                                                                                                                               92WO-GB001570
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 85.6
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-100978/12
                                                                                                                                                                                                                                                                                                                                                                              Vanderleyden J;
                                                                                                                                                                                                                                                                                                                                                       Broekaert WF,
                                                                                                                                                                                                                      29-AUG-1991;
13-FEB-1992;
25-JUN-1992;
                                                                                                                                                                               27-AUG-1992;
                                                                                        WO9305153-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
14-FEB-1995
                                                                                                                                    L8-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 AAGTIGIGGGAGAAGCCAAGIGGGACAIGGICAGGGGITIGGGGAAACAGTAAIGCAIGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 AAGAATCAGTGCATTAACCTTGAAGGAGCCAAACATGGATCATGCAACTATGTCTTCCCA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes the Arabidopsis PDF1.2 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                                                                                                                                Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGITGIGCGAGAGACCAAGIGGGACATGGICAGGAGTITGIGGGAACAATGCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

76.5%; Score 117.8; DB 2; Length
Best Local Similarity 85.6%; Pred. No. 5.4e-30;
Matches 131; Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcacacaagrerarcrerracerccarerraa 274
                                                                                        /*tag= c
/product= "PDF1.2"
/note= "plant defensin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 72pp; English.
                                                                                                                                                                                                                                                                     97WO-GB001672
                                                                                                                                                                                                                                                                                                                 96GB-00013753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                         32. .119
/*tag= b
120. .271
         *tag=
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                                                                                                                                                                                                                                                                                                                                                            (ZENE ) ZENECA LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW40346
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07-JUL-1993
                                                                                                                                                                                                                                                                        20-JUN-1997;
                                                                                                                                                                                                                                                                                                                 01-JUL-1996;
                                                                                                                                                                                   WO9800023-A2
                             sig_peptide
                                                                      mat_peptide
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Kazan K;

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AAQ38650;

RESULT 13 AAQ38650

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Gaps ö transl except= (pos:85. .87, aa:Glu)

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symbiosis; disease-resistance; fungus-resistance; cynodontis; Cxc; crop improvement; endophyte; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA sequence of Rs-AFP1 is given in AAQ70128. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                 Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.5%; Score 117.8; DB 2; Length 414; 85.6%; Pred. No. 5.5e-30; ive 0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 31; 39pp; English
                                                                                                                                                                                                                                                                         SB;
                                                                                                                                                                                                                                                                         ReeB
                                                                                                                                                                          94WO-GB000012
                                                                                                                                                                                                         93GB-00000281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.6°
Matches 131; Conservative
                            Antimicrobial; Rs-AFP1;
Clavibacter xyli subsp.
                                                                                                                                                                                                                                                                      Powell KA,
Antimicrobial Rs-AFP1,
                                                                                                                                                                                                                                                                                                     WPI; 1994-249223/30.
                                                                                                                                                                                                                                         (ZENE ) ZENECA LTD
                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR57325
                                                                              Raphanus sativus
                                                                                                                                                                          05-JAN-1994;
                                                                                                                                                                                                         38-JAN-1993;
                                                                                                            WO9416076-A1
                                                                                                                                                                                                                                                                         Dubock AC,
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                                                                                                                 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                        166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 225
                                          61
                                                                      106 AAGTTGTGCGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC
                                      2 AGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGIITGIGGGAACAACAAIGCAIGC
  Gaps
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                                                                                                                                                                                                                                         226 GCTCACAAGTGTATCTGCTACTTTCCTTGTTAA 258
                                                                                                                                                                                                GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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Antifungal protein; candida; fungal resistance; food additive; radish; crop protection; plant defensin; bacterial protection; preservative; ss.
                                                                                                  Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.
                    AAT72333 standard; cDNA; 414
                                                                            (first entry)
                                                                 (revised)
                                                               25-MAR-2003
19-JAN-1998
                                          AAT72333;
RESULT 15
         AAT72333
```

Location/Qualifiers 16. .258 /\*tag= a

Raphanus sativus.

Search completed: May 18, 2004, 17:22:40 Job time: 151.15 secs

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Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This cDNA sequence encodes an Rhapanus sativus (radish) antifungal protein (Rs-AFP1). Analogues of the homologous protein, Rs-AFP2 (AAM19281), have also been produced (see AAM1928292, AAM1928194, AAM19310-104, AAM19330-34 and AAW17165-834). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease tolerance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGITIGIGGGAACAACAAIGCAIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                         Sijtsma L, Van Amerongen A;
Borremans FAM, Rees SB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.5%; Score 117.8; DB 2; Best Local Similarity 85.6%; Pred. No. 5.5e-30; Matches 131; Conservative 0; Mismatches 22;
                                                                                   "antifungal_protein_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dereacadereraterecraetricerierian 258
                                                                                                                                                                                                                                                                                                         Puijk WC, Schaaper WMM,
1, Samblanx GW, Fant F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Fig 2; 65pp; English.
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P-PSDB; AAW19280.
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Broekaert W, San
Van Gelder WMJ;
                                                                                                                                                                                                                                        28-MAR-1996;
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              sig_peptide
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                                              mat_peptide
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Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 154; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/627,706
US-09-103-489-17
US-09-829-381D-17
US-08-377-687-50
US-08-971-982-50
US-08-971-982-50
US-08-977-687-33
US-08-377-687-33
US-08-377-687-33
US-08-377-687-33
US-08-377-192-33
US-08-977-192-33
US-08-971-982-33
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US-08-971-982-34
US-08-971-982-34
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CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: COhen, Charles E. REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700) A TELEPHONE: (314)537-624
ITELEPHONE: (314)537-6047
INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 270 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-777-192-36
US-08-971-982-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-627-706-14; Sequence 14, Application US/08627706; Patent No. 5773696
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CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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Sequence 12,
Sequence 12,
Sequence 12,
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Sequence 48,
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1 aaggttgtgcgagagaccaa......tttgttacttcccatgttaa 154
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    /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
    /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
    /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-829-381D-14
US-08-627-381D-12
US-09-103-489-12
US-09-103-489-9
US-09-829-381D-12
US-09-829-381D-12
US-09-829-381D-9
US-08-377-687-48
US-08-377-687-48
US-08-971-982-48
US-08-971-982-48
US-09-077-948-45
US-09-077-948-45
US-09-103-489-5
US-09-829-381D-5
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US-08-971-982-58
US-08-971-982-58
US-08-929-381D-8
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US-09-829-381D-16
US-08-627-706-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           682709 seqs, 277475446 residues
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                                                                                                                                                                                                                                                                                                                                               US-10-681-972-12_COPY_116_269
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Listing first 45 summaries
                                                                                                                                                               - nucleic search, using sw model
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Maximum DB
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APPLICANT: Shab, Dilip M.
APPLICANT: Shab, Dilip M.
APPLICANT: Shab, Dilip M.
APPLICANT: Shab, Dilip M.
APPLICANT: Shab, Dilip M.
APPLICANT: Wound M.
APPLICANT: Womenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
FILE REFERENCE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AAGGTIGIGCGAGAGCCAAGTGGGACAIGGTCAGGAGTTIGIGGGAACAACAATGCAIG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC
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Patent No. 5773696

GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Bhah, Dilip M.
APPLICANT: Bhah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF ENGRESPONDENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 154; DB 4; Length 2'
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 154; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Data PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: COCHEN, Charles E.
REGISTRATION NUMBER: 34,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AGCTCACAAATGTATTTTGTTACTTCCCATGTTAA 154
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                    Sequence 14, Application US/09829381D Patent No. 6653280 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: Plasmid US-09-829-381D-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-08-627-706-12
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                                                                                  108 AAGGTTGTGCGAGAGCCAAGTGGGACATGGTCAGGAGTTTGTGGGGAACAACAATGCATG 167
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108 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 167
                                                        CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC
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Sequence 14, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F STREET: 700 Chesterfield Village Parkway No. 6215048th CITY: St. Louis STATE: Missouri COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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2IP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UNA-1998
CLASSIFICATION *800
ATTORNEY/ABENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 34.565
TELEPHONE: (314) 537-624
TELEPHONE: (314) 537-624
TELEFROM: (314) 537-6047
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 154; DB 3; Best Local Similarity 100.0%; Pred. No. 2.8e-42; Matches 154; Conservative 0; Mismatches 0;
                                                                                                                                                                  121 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: CDNA
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US-08-627-706-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09103489

Patent No. 6215048

GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Roenberger, Cindy A.
TITLE OF INVENTION: Controlling Plant Pathode for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 70 Chesterfield Village Parkway No. 6215048th
                                                                                                                                                                                                                                                                                                                                      ·,
                                                                                                                                                                                                                                                                                      100.0%; Score 154; DB 1; Length 286; 100.0%; Pred. No. 2.9e-42; tive 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UNV-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: COHEN, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 269
      38-21 (10700) A
REFERENCE/DOCKET NUMBER: 38-2
TELECPHONE: (314)537-6224
TELEPHONE: (314)537-6224
TELEPAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (314) 537-6224
TELEPAX: (314) 537-6447
INPERMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 286 base pairs
TYPE: nucleic acid
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ZIP: 63198
COMPUTER READABLE FORM:
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TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 154;
                                                                                                                                                                                                                                             US-08-627-706-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-103-489-12
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GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
PRIOR RILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAGGTTGTGCGAGAGCCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG
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                                                            ;
0
        Length 286;
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Patent No. 5773696
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
Query Match
Best Local Similarity 100.0%; Pred. No. 2.9e-42;
Matches 154; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 154; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.9e-42;
Matches 154; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic PCR reaction product
                                                                                                                                                                                                                                                                                                                                                                236 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 269
                                                                                                                                                                                                                                                                                                                                 121 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AGCICACAAAIGIATITGITACTICCCATGITAA 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/09829381D Patent No. 6653280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-09-829-381D-12
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles B.
REGISTRATION NUMBER: 34.565
REPERENCE/DOCKET NUMBER: 38-21 (1070
TELECOMMUNICATION INFORMATION:
TELEFAN: (314) 537-624
TELEFAN: (314) 537-624
TELEFAN: (314) 537-624
TELEFAN: (314) 537-624
TELEFAN: (314) 537-624
TELEFAN: (314) 537-624
TELEFAN: (314) 537-6497
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
i LOCATION: (22)...(22)
i OTHER INFORMATION: N = any nucleotide
US-09-829-381D-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09829381D Patent No. 6653280
                                                                                                                                                                                                                                                                                                                        LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-09-103-489-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Alyssum spp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-829-381D-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.0%; Score 140.2; DB 1; Length 500; 94.8%; Pred. No. 1.4e-37; tive 0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09103489

Patent No. 6215048

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rounie S.
ITILE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
OORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Charles E. Cohen, Monsanto Company, BB4F 700 Chesterfield Village Parkway No. 6215048th
          CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
FILING DATE:
ATTONEY/AGENT INFORMATION:
NAME: COCHEN, Charles E.
REGISTRATION NUMBER: 34,565
REGISTRATION NUMBER: 34,565
REGISTRATION NUMBER: 34,565
REGISTRATION NUMBER: 314,565
REGISTRATION STATION:
TELEPHONE: (314)537-6224
TELEPHONE: (314)537-6224
JINFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
TWOTH. 600 DASSE PATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: I BROOPY disk
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 94.8
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 700 Chest
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                    St. Louis
Missouri
                                                                                 CITY: St. LASTATE: MiBBACOUNTRY: US. ZIP: 63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-627-706-9
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Parent No. 655280
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Bhah, Dilip M.
APPLICANT: Womenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REPERENCE: 38-21 (10700) Pathogenic Fungi
FILE REPERENCE: 38-21 (10700) Pathogenic Fungi
FILE REPERENCE: 138-21 (10700) Pathogenic Fungi
FILE REPERENCE: 198-104-109
FRIOR APPLICATION NUMBER: 02/01-03,489
FRIOR APPLICATION NUMBER: 09-04-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 500
                                                                                                                                                                                                                     159 AAGTIGIGGAAGAGTCCAAGTGGAACATGGTCAGGCGTGTGTGGGAATAATAACGCATGC 218
                                                                                                                                                                                                                                                                                                                                             219 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACAGGGATCTTGCAACTATGTCTTCCCA 278
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                                                                                                                                                   0; Gaps
                                                                             Gaps
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   DB 3; Length 500;
Query Match 91.0%; Score 140.2; DB 3; Length Best Local Similarity 94.8%; Pred. No. 1.4e-37; Matches 145; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 GCTCACAATGTATTTGTTACTTCCCATGTTAA 311
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70 171 11

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62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

76.5%; Score 117.8; DB 1; Length 414;
Best Local Similarity 85.6%; Pred. No. 4.2e-30;
Matches 131; Conservative 0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECHMONICATION INFORMATION:
TELEFAX: 202-861-3000
TELEFAX: 202-861-3000
TELEFAX: 202-82-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHRACTERISTICS:
LENGTH: 414 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
226 GCTCACAAGTGTATCTGCTACTTTCCTTGTTAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
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       RESULT 11
US-08-777-192-48

; Sequence 48, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
    APPLICANT: CAMMUE, BRUNO P.A.
    APPLICANT: CAMMUE, BRUNO P.A.
    APPLICANT: TERRAS, FRANKY R.G.
    APPLICANT: TERRAS, FRANKY R.G.
    APPLICANT: TERRAS, FRANKY R.G.
    APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSE:
    STREET:
    STREET:
                                                                                                                                                                                                                                                                                                                                                                            STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
US-08-777-192-48
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                                          219 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 278
  AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:

CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISCHATION NUMBER: 16,773
REFERRICE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELEPHONIS: 202-861-3000
TELEPHONIS: 202-861-3000
TELEPHONIS: 202-861-3000
TELEPHONIS: 202-861-3000
TELEPHONIS: 202-81-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
                                                                                         122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                   GENERAL INCRMATION:
APPLICANT: BROEKABET, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: TERRAS, FRANK W.
APPLICANT: TERRAS, FRANK R.G.
APPLICANT: TERRAS, FRANK R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CUSHWAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                               US-08-377-687-48
; Sequence 48, Application US/08377687
; Patent No. 5538525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 414 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16..255
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US-08-377-687-48
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62
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                                                                                                                                                                                                                                                                                                                                                                        COMPUTRY: USA

ZIP: 2005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CURENT APPLICATION NAMER: US/08/971.982

FILING DATE: 17-No. 6187904-1997

CLASSIFICATION NAMER: US/08/971.982

PRIOR APPLICATION NAMER: US 08/002,480

FILING DATE: 04-JAN-1993

ATPANES AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 16,773

TELEPRA: 202-861-3000

TELEPRA: 202-861-3004
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                                                                                                                                            REES, SARAH B.
THERRAKY R.G.
VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS: ADDRESSE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 16..255
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                                                                               APPLICANT: BROEKAERT, WILLEM F. CAMMUE, BRUNO P.A. OSBORN, RUPERT W.
               Sequence 48, Application US/08971982 Patent No. 6187904 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGHT: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                               STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
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US-08-971-982-48
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RESULT 13
US-09-077-951-19
Sequence 19, Application US/09077951
Fatent No. 6372888
GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.5%; Score 117.8; DB 4; Length Best Local Similarity 85.6%; Pred. No. 4.2e-30; Matches 131; Conservative 0; Mismatches 22; Indels
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APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
TITLE CANTERES. Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REPERENCE: PED50093
CURRENT APPLICATION NUMBER: US/09/077,951
CURRENT FILING DATE: 1999-31.1
EARLIER APPLICATION NUMBER: GB 9525474.4
EARLIER PILING DATE: 1995-12-13
EARLIER PILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/GB96/03068
PRIOR FILING DATE: 1996-12-12
PRIOR APPLICATION NUMBER: GB 9606552.9
PRIOR PILING DATE: 1996-03-28
PRIOR APPLICATION NUMBER: GB 9525455.3
PRIOR FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 45
LENGTH: 414
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THE REPRENCE: 108946-257 (SYM-035)
CURRENT APPLICATION NUMBER: US/09/077,948A
CURRENT FILING DATE: 1998-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 45, Application US/09077948A
Patent No. 6605698
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Borremans, Frans
De Samblanx, Genoveva
Sitjtsma, Lolke
Meloen, Robbert
Puijk, Wouter
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APPLICANT: Schaaper, Wilhelmus
APPLICANT: Brockaert, Willem
APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Rees, Sarah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Van Amerongen, Aart
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; ORGANISM: Raphanus sativus
US-09-077-948A-45
                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Raphanus sativus
US-09-077-951-19
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US-09-077-948A-45
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completed: May 18, 2004, 19:02:19

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62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Woenser, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Challes E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 63198
ZIP: 63198
ZIP: 63198
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn'Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
                                                                                                                                                                                                  226 GCTCACAAGIGTATCTGCTACTTTCCTTGTTAA 258
                                                                                                                                                                         122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICALLE
FILING DATE:
FILING DATE:
CLASSIPICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
"FILEFAK: (314)537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCACAGAGGCATATGCTACTTCCCCTGT 308
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                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08627706
Patent No. 5773696
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 308 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.3
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 700 Chest
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE:
US-08-627-706-5
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Sequence 9, Applisequence 13, Applisequence 2046, Apsequence 2046, Apsequence 15, Applisequence 607, Applisequence 45, Applisequence 45, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, Applisequence 19, A
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Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 9, Appli
                                                                                                                                                                                         (without alignments)
4930.226 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                  1 aaggttgtgcgagagaccaa......tttgttacttcccatgttaa 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          May 18, 2004, 17:59:12 ; Search time 141.75 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5894648
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-732-561-15
US-09-887-576-607
US-09-759-584-48
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US-09-732-561-13
US-09-938-842A-2046
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US-09-829-381A-12
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US-09-829-381A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2947324 segs, 2269024515 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                            US-10-681-972-12_COPY_116_269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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76.5
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1190.2
1119.4
1117.8
1117.8
1117.8
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                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                  Run on:
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No.
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-732-561 -829-381 -681-97 -759-584	3 US-10-681-97 US-09-829-381 3 US-10-681-97 US-09-829-381 3 US-10-681-97	US-09 US-09 5 US-1	S US-10 S US-10 S US-10 S US-10	5 US-1 5 US-1 5 US-1 5 US-1 5 US-1	15 US-10-178-449A-5 9 US-09-759-584-31 9 US-09-759-584-34 9 US-09-759-584-34 15 US-10-178-449A-48 15 US-10-178-449A-31
1616 308 308 288 306	306 285 285 285 285	284 373 156 610	65 4 4 4 4 6 5 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	464 472 603 461 565	501 150 150 150 529
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116.2 115.4 115.4 113	110.6 109.2 109.2 102.8	77 4 4 4 6 8 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	444444 ECCCCC	4 4 4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6	4 . W . W . W . W . W . W . W . W . W .
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## ALIGNMENTS

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                     APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION AURENER: 09/103,489
FILING DATE: 1998-06-24
ATTOREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
                           Sequence 14, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 63198
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                      CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
US-09-829-381A-14
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US-10-388-361A-45 US-10-006-252A-19

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                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
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                                                                                                                                          APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 286;
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MEDIUM TYPE: Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Eclease #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CIASSIFICATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGEN THORMATION:
NAME: COMPON. CAPALES E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INPERR: 38-21 (10700)A
TELECOMMUNICATION INPERR: 38-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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100.0%; Pred. No. 2.4e-42;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: CDNA; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-829-381A-12
                                                                        ; Sequence 12, Application US/09829381A; Patent No. US20020144306A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/10681972; Publication No. US20040064850A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 286 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 154; Conservative
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APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 63198
                                          US-09-829-381A-12
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GENERAL INVENTALION:

APPLICANT: Shah, Dilip M.

APPLICANT: Shah, Dilip M.

APPLICANT: Shah, Dilip M.

APPLICANT: Shah, Dilip M.

APPLICANT: Rosenberger, Cindy A.

TILE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contro;

TILLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for CONTRO!

TILLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for CONTRO!

TILLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for CONTRO!

TILLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for CONTRO!

CURRENT FILING DATE: 2003-10-09

PRIOR FILING DATE: 2001-04-09

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Version 3.1

SEQ ID NO 14

LENGTH: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 227
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                                                                                                                                                                                                                                                                                                                                 Length 270;
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                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 154; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.3e-42;
Matches 154; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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TELEFAX: (314) 537-6047

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: muclaic acid
STRANDEDNESS: single
TYPE: TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-829-381A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Plasmid
US-10-681-972-14
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US-10-681-972-14
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APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Will Younde S.
APPLICANT: Will Younde S.
APPLICANT: Will Younde S.
TITLE OF INVENTION: Palant Pathogenic Fungi
FILLE OF INVENTION: Plant Pathogenic Fungi
FILLE OF INVENTION: Plant Pathogenic Fungi
FILLE DATE: 2003-10-09
CURRENT APPLICATION NUMBER: US/10/681, 972
CURRENT APPLICATION NUMBER: US/09/829,381D
PRIOR FILLING DATE: 2001-04-09
PRIOR FILLING DATE: 2001-04-09
PRIOR FILLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                       Length 500;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                       91.0%; Score 140.2; DB 9;
94.8%; Pred. No. 1.6e-37;
live 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.0%; Score 140.2; DB 13;
94.8%; Pred. No. 1.6e-37;
Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 GCTCACAATGTATTTGTTACTTCCCATGTTAA 311
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                                                                                                                                                                                                      MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-829-381A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: N = any nucleotide US-10-681-972-9
       TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.8
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 91.0
Best Local Similarity 94.8
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc feature
LOCATION: (22)..(22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Alyssum spp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-10-681-972-9
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LENGIH: 500
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APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyseum and Methods for Contro TITLE OF INVENTION: Plant Pathogenic Fungi FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT APPLICATION NUMBER: US/09/829,381D
PRIOR PILING DATE: 2003-10-09
PRIOR PLING DATE: 2001-04-09
PRIOR PLING DATE: 2001-04-09
PRIOR PLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARER: Patentin Version 3:1
ERNGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 AAGGTTGTGCGAGAGCAAGTGGGACATGGTCAGGAGTTTGTGTGGGAACAACAATGCATG 175
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ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGITIGIGGGAACAAIGCAIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 286;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 154; DB 13; Best Local Similarity 100.0%; Pred. No. 2.4e-42; Matches 154; Conservative 0; Mismatches 0;
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REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Synthetic PCR reaction product
US-10-681-972-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 269
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-06-24 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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COMPUTER READABLE FORM:
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STATE: Missouri
COUNTRY: USA
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US-09-829-381A-9
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Sequence 2046, Application US/09938842A

Batent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Joeff

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Same, AND METHODS OF USE

TITLE OF INVENTION: Same, AND METHODS OF USE

TITLE OF INVENTION: Same, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION NUMBER: US/09/938, 842A

CURRENT FILING DATE: 2000-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR PLING DATE: 2001-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: S379

SEQ ID NO 2046

LENGTH: 243
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76.5%; Score 117.8; DB 9; Length
Best Local Similarity 85.6%; Pred. No. 5.3e-30;
Matches 131; Conservative 0; Mismatches 22; Indels
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2046
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US-09-938-842A-2046
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  US-09-938-842A-2046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
FLING DATE:
CLASSIFICATION: DATA:
PRIOR APPLICATION NUMBER: 09/202,638
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279 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 311
                                                                                                                                                                                      APPLICANT: Thomma, Bart
APPLICANT: Thorma, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Kazan, Kemal
APPLICANT: Broekaert, Willem
APPLICANT: Broekaert, Willem
APPLICANT: Broekaert, Willem
APPLICANT: Broekaert, Willem
APPLICANT: Plant Protection Method
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: HOADMAGALE, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECHOME: (302) 886-1699
INFORMATION FOR SEQ ID NO: 13:
SEQUENCH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                             US-09-732-561-13
; Sequence 13, Application US/09732561
; Patent No. US20020035738A1
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA AG Products
STREET: 1800 Concord Pike
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ilarity 86.3%;
Conservative (
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STATE: DE
COUNTRY: USA
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Best Local Similarity
Matches 132; Conserv
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                                                                                                                                                                  GENERAL INFORMATION:
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MOLECULE TYPE: C
ORIGINAL SOURCE:
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RESULT

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                                                    62 AGGNACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Best Local Similarity 85.6
Matches 131; Conservative
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62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: Chang, H.
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Pred. No. 6.5e-30;
0; Mismatches 22;
                                                                                                                                                                                                   242 GCACACAGIGIAICIGITACGICCCAIGITAA 274
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                                                                                                                                     122 GCTCACAAAIGTATTTGTTACTTCCCATGTTAA 154
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PRIOR APPLICATION NUMBER: US 60/213,848

PRIOR FILING DATE: 2000-06-23

PRIOR PRILICATION NUMBER: US 60/214,087

PRIOR PELICATION NUMBER: US 60/214,087

PRIOR PELICATION NUMBER: US 60/258,692

PRIOR PELICATION NUMBER: US 60/258,692

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 875

SOFTWARE: FastSEQ for Windows Version 4.0

: ERNORT: A.C.
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; Patent No. USZ0010014732A1
; GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: TERES, SARAH B.
APPLICANT: TERES, FRANKY R.G.
APPLICANT: TERES, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                             Sequence 607, Application US/09887576
Patent No. US20020144047A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(400)
; OTHER INFORMATION: n = A,T,C
US-09-887-576-607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.6%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                     US-09-887-576-607
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US-09-759-584-48
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                                                                                                                                                                    151 AAGAATCAGTGCATTAACCTTGAAGGAGCCAAACATGGATCATGCAACTATGTCTTCCCA 210
                                                          91 AAGTIGIGGAGAAGCCAAGIGGACAIGGICAGGGGITIGCGGAAACAGIAAIGCAIGC 150
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   TGTGGGAACAACAATGCATGC
                                                                                                                              62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
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Pred. No. 6.5e-30;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/09732561
Fatent No. US20020035738A1
GENERAL INFORMATION:
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  211 GCACACAAGTGTATCTGTTACGTCCCATGTTAA 243
                                                                                                                                                                                                                                                             122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/732,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PARIOR APPLICATION DATA:
PAPLICATION NUMBER: 09/202,638
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: ZENECA AG Products
I: 1800 Concord Pike
Wilmington
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Best Local Similarity 85.6%;
Matches 131; Conservative
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COMPUTER READABLE FORM:
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ORIGINAL SOURCE:
STRAIN: PDF1.2
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STREET: 18
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US-09-732-561-15
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166 AAGAATCAGTGCATTAACCTTGAGAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 AGGAACCAAIGCAGAAACCTIGAAAGAGCAGAACAGGAICTIGCAACTAIGTCTICCCA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 414;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.5%; Score 117.8; DB 13; Length Best Local Similarity 85.6%; Pred. No. 6.6e-30; Matches 131; Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.5%; Score 117.8; DB 14; Length 85.6%; Pred. No. 6.6e-30; Live 0; Mismatches 22; Indels
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                         CURRENT APPLICATION NUMBER: US/10/388,361A
CURRENT FILING DATE: 2003-03-13
PRIOR PRILICATION NUMBER: US 09/077,948
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1995-12-13
SCFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaert, Willem
APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SIN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 2001-12-04
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 77
SECTRARRE: Patentin Ver. 2.0
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Publication No. US20020152498A1
      FILE REFERENCE: 50094PPDDIV
                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Raphanus sativus
US-10-388-361A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA; ORGANISM: Raphanus sativus
US-10-006-252A-19
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Best Local Similarity
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                                                                                                                                                 ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99042/SEE.36525/US/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 GCTCACAAGTGTATCTGCTACTTTCCTTGTTAA 258
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN DARBY & CUSHWAN STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Antifungal Proteins
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCY DOCKET NUMBER: 99042/S:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45, Application US/10388361A
Publication No. US20030226169A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: mucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
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Broekaert, Willem
Van Gelder, Wilhelmus
Rees, Sarah
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Sitjtsma, Lolke
Meloen, Robbert
Puijk, Wouter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Van Amerongen, Aart
APPLICANT: Fant, Franky
APPLICANT: Borremans, Frans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
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LOCATION: 16..255
                                                                                       WASHINGTON
                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-388-361A-45
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                                                                                                                                   COUNTRY:
                                                                                       CITY: W
STATE:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/GB97/01672
FILING DATE:
APPLICATION NUMBER: BCT/GB97/01672
FILING DATE:
APPLICATION NUMBER: 33,712
REPERENCY DOCKET NUMBER: 33,712
REFERENCY DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SED ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1616 base pairs
TYPE: nucleic acid
STRANDEDRESS: single
                                                                                                                                                                                                                                  APPLICANT: Terras, Franky
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Kazan, Kemal
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSE:
ADDRESSEE: ZENECA AG Products
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
STATE: DE
  122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                         226 GCTCACAAGTGTATCTGCTACTTTCCTTGTTAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 GCTCACAAATGTATTGTTACTTCCCATGTTAA 154
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MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

STRAIN: Arabidopsis PDF1.2 gene

INDIVIDUAL ISOLATE: DNA sequence Figure 14
US-09-732-561-21
                                                                                                                                                                   Sequence 21, Application US/09732561
Patent No. US20020035738A1
                                                                                                                                                                                                                   GENERAL INFORMATION:
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1535 GCACACAAGTGTATCTGTTACGTCCCATGTTAA 1567
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Search completed: May 18, 2004, 20:33:21 Job time : 141.75 secs man min min min m

Sequence:

Title:

Run on:

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Searched:

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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100:
101:
102:
104:
104:
106:
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 (without alignments) 3225.394 Million cell updates/sec
                                             1 aaggitgiggagagaccaa......ttigitacitcccatgitaa 154
                                                                                                May 18, 2004, 17:15:17; Search time 1680 Seconds
   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                              37577330 seqs, 17593059518 residues
                                                                     hits satisfying chosen parameters:
                                      US-10-681-972-12_COPY_116_269
                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                 nucleic search, using sw model
                                                    IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                         Perfect score:
                                                    Scoring table:
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                 nucleic
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SUMMARIES

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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Why Younie W.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REPERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Version 3.1
SEQ ID NO 12
LENGTE: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 120
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100.0%; Pred. No. 7.1e-39;
tive 0; Mismatches 0;
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                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                     ; OTHER INFORMATION: Plasmid US-10-681-972-14
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 154; Conservative
SEQ ID NO 14
LENGTH: 270
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APPLICANT: Shah, Dilip M.

APPLICANT: Shah, Dilip M.

APPLICANT: Shah, Dilip M.

APPLICANT: White M. Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah, Shah
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13, Appl
117133,
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Sequence 19, Appl
Sequence 45, Appl
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Sequence 48, Appl
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US-09-935-625-5383
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US-10-006-252A-19
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                                                                               DB
                                                                               Length
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Gaps

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APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
LENGTH: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELLS, AND METHODS THEREOF CAPABLE
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                                                                                           210
              91 AAGTIGIGCGAGAAGCCAAGIGGIACTIGGICAGGAGTTIGCGGAAACAGCAAIGCAIGC 150
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TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES,
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
TILLE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.6%; Score 122.6; DB 36
87.6%; Pred. No. 9.8e-29;
Live 0; Mismatches 19,
                                                                                                                                                     122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                   211 GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 243
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NAME/KEY: Misc_feature
LOCATION: 1..243
CHER INFORMATION: Ceres Seq. ID no. 2711695
US-09-935-625-5383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Ceres Seq. ID no. 2143607
US-09-935-625-5250
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                                                                                                                                                                                                                                                                                                             Sequence 5250, Application US/09935625 GENERAL INFORMATION:
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Best Local Similarity 87.6'
Matches 134; Conservative
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Matches 134; Conserva
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US-09-935-625-5383
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LENGTH: 243
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyseum and Methods for Contror TITLE OF INVENTION: Plant Pathogenic Pungi
TITLE OF INVENTION: Altifungal Polypeptide ALYAFP from Alyseum and Methods for Contror TITLE OF INVENTION: DIABLE: 2003-10-09
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT APPLICATION NUMBER: US/09/829,381D
PRIOR PLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 500
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 18199
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Pred. No. 2.5e-34;
0; Mismatches 8; Indels 0;
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NAME/KEY: misc feature

LOCATION: 1..243

OTHER INFORMATION: any n = a, g, c, t, unknown, or other

NAME/KEY: misc feature

LOCATION: 1..243

OTHER INFORMATION: Ceres Seq. ID 1833757

US-09-708-427-18199
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; OTHER INFORMATION: N = any nucleotide
US-10-681-972-9
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 94.8%;
Matches 145; Conservative
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ORGANISM: Alyssum spp
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. USSN 60/120,645 1999-02-18; USSN 09/443,025 1999-11-1; USSN 60/120,645 1999-02-18; USSN 09/443,025 1999-11-12;
                                                                                                                                       151 AAGAATCAGIGCATTAACCTTGAAGGAGCAAAACATGGATCTTGCAACTATGTCTTCCCA 210
                                                                                                                                                                                      62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                                                             2 AGGITGIGCGAGAGCCAAGIGGGACAIGGICAGGAGTITGIGGGAACAACAAIGCAIGC
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                                                      Gaps
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TITLE OF INVENTION: Plant Genome Sequences and Uses Thereof
FILE REPERBNCE: 38-10(15478)B
CURRENT PAPLICATION NUMBER: US/09/505,532
CURRENT FILING DATE: 200-0-16
PRIOR APPLICATION NUMBER: USSN 60/120,645 1999-02-18; USSN 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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  Score 122.6; DB 38; Length 243; Pred. No. 9.8e-29; 0; Mismatches 19; Indels 0;
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Query Match

Post 122.6; DB 21; Length 584;
Best Local Similarity 87.6%; Pred. No. 1.3e-28;
Matches 134; Conservative 0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cac, Yongwei
APPLICANT: Timberlake, William E.
TITLE OF INVENTION: Plant Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15478) B
CURRENT FILIOR DATE: US/09/819,091A
CURRENT FILIOR DATE: 1900-02-16
PRIOR APPLICATION NUMBER: US 60/108,420
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: US 60/120,645
PRIOR APPLICATION NUMBER: US 60/120,645
PRIOR APPLICATION NUMBER: US 09/443,025
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 51470
                                                                                                                                                                                                                                                                                                                           211 GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 243
                                                                                                                                                                                                                                                                                    122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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10.09-819-091A-7439/c

i Sequence 7439, Application US/09819091A

i GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
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; ORGANISM: Arabidopsis thaliana
US-09-505-532-7439
Query Match 79.6%;
Best Local Similarity 87.6%;
Matches 134; Conservative
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SEQ ID NO 7439
LENGTH: 584
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LENGTH: 584
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
TITLE OF INVENTION: MODILATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
URRENT APPLICATION NUMBER: 2010-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 28943
                                                                                                                                                                                                                                                                                                                                                                                                                                               CELLS, AND METHODS THEREOF CAPABLE
                                                                                                                                            62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                                                                                                                                                                                                                                                                                                                              Sequence 28557, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNCLECTIDES, POLYPEPTIDES,
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES;
FILE REFERENCE: 2750-1481P;
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 28557
LENGTH: 243
                 2 AGGTTGTGCGAGACCAAGTGGGACATGGTCAGGAGT
                                                                                                                                                                                                                                     211 GCTCACAAGIGTATCTGTTACGTCCCAIGTTAA 243
                                                                                                                                                                                                       122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
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LOCATION: 1..243

JOHER INFORMATION: Ceres Seq. ID no. 2143607

US-09-935-625-28557
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; LOCATION: 1...243
; LOCATION: Ceres Seq. ID no. 2711695
US-09-935-625-28943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Arabidopsis thaliana
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Best Local Similarity 87.6%;
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US-09-935-625-28557
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TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Bush, David F.
APPLICANT: Levin, Irena M.
APPLICANT: Levin, Irena M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Roundsley, Steven D.
APPLICANT: Roundsley, Steven D.
APPLICANT: Wiegand, Roger C.
ITLE OF INVENTION: PLANT POLYMORPHIC MARKERS AND USES THEREOF FILLS REPRENCE: 38-10(15493)B
CURRENT APPLICATION NUMBER: US/09/534,859
CURRENT FILING DATE: 2000-229
1000 The CORRENT FILING DATE: 2000-229
11177
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                                                          79.6%; Score 122.6; DB 33; Length 584; 87.6%; Pred. No. 1.3e-28; tive 0; Mismatches 19; Indels 0;
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APPLICANT: Levin, Irena M.
APPLICANT: Nouris, Susan R.
APPLICANT: Nounsley, Steven D.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof FILE REPERENCE: 38-10(15493) D.
CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT PILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/534,859
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Pred. No. 6.2e-28;
0; Mismatches 19; Indels
                                                                                                                                               2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTT
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ORGANISM: Arabidopsis thaliana
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; ORGANISM: Arabidopsis thaliana
US-09-534-859-830
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Best Local Similarity 87.6%;
Matches 134; Conservative (
                                                                              Best Local Similarity 87.6
Matches 134; Conservative
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    ; ORGANISM: AFADIC
US-09-819-091A-7439
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LENGTH: 61290
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: identified by Attorney Docket number 04983.0206CPUS01 38-10-
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 1582
                                                                                                                                                                                                                                                                                                                                                                                                    22689 AAGTIGIGGGAGAAGCCAAGIGGGACATGGTCAGGCGTTTGCGGAAACAGTAATGCATGC 22630
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APPLICANT: Levin, Irena M.
APPLICANT: Levin, Irena M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Rounsley, Steven D.
APPLICANT: Wiegand, Roger C.
ITLE OF INVENTION: 38-10(15493)B
CURRENT APPLICATION NUMBER: US/09/534,859
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 1127
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; Sequence 284, Application US/09803736
; GENERAL INFORMATION:
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US-09-803-736-830
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Best Local Similarity 87.6'
Matches 134; Conservative
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                                                                                        SEQ ID NO 830
LENGTH: 61290
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APPLICANT: Rounsley, Steven D.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
FILE REPERENCE: 38-10(15.493)D
CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 12000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-10-20
PRIOR SEQ ID NOS: 1582
SEQ ID NO 284
LIENGTH: 87080
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S ESQUENCE 21472. Application US/09708427

S ESQUENCE 21472. Application US/09708427

GENERAL INFORMATION:

TICKEN OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

TITLE OF INVENTION: 2750-1243P

CURRENT APPLICATION WINDER: US/09/708,427

CURRENT APPLICATION WINDER: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

S SOFTWARE: Patentin version 3.1

SEQ ID NO 21472
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LOCATION: 1..243
COTHER INFORMATION: any n = a, g, c, t, unknown, or other
NAME/KEY: misc feature
LOCATION: 1..243
COTHER INFORMATION: Ceres Seq. ID 1839548
US-09-708-427-21472
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                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-284
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Best Local Similarity 66.39
Matches 132; Conservative
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GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154

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Search completed: May 18, 2004, 20:22:42 Job time : 1681 secs

211 GCTCACAAGTGTATCTGTTACTTCCCATGTTAA 243

us-10-681-972-12 copy 116 269. rnpn

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RESULT 2
US-10-417-375A-151/c
US-10-417-375A-151/c
Sequence 151, Application US/10417375A
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE REPERENCE: 529452001600
GURRENT APPLICATION UNMER: US/10/417,375A
CURRENT FILING DATE: 2003-04-15
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4: /cgn2-6/ptodateJ/L/pna/USO8 NEW COMB.seq:*

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FEATURE:

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LOCATION: (1)...(163548)

OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-:
US-10-767-471-10730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CARGILL,
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ABBUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOLSOS
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT PILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FASLERQ for Windows Version 4.0
SEQ ID NO 10730
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GRNERAL INFORMATION:
APPLICANT: CARGILL.
AITLE CARFILL.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FateSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.5%; Score 34.6; DB 6; Length 42063; 59.8%; Pred. No. 0.26; Live 0; Mismatches 39; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-417-375B-151/c

Sequence 151, Application US/10417375B
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
FILE REFERENCE: 5295200160;
CURRENT APPLICATION NUMBER: US/10/417,375B
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 151
INSTRUCTH: 42063
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                                                                                                                                                                                                                                                                                                                                                                                                                           61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACAC 97
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NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 151
LENGTH: 42063
                                                                                                                                                                    ; LOCATION: (1)....(42063)
; OTHER INFORMATION: n = A,T,C or G
US-10-417-375A-151
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; NAME/KEY: misc feature
LOCATION: (1)...(42063)
; CTHER INFORMATION: n = A,T,C or G
US-10-417-375B-151
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Best Local Similarity 59.84
Matches 58, Conservative
                                                                                    TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                  NAME/KEY: misc feature
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                                                              Gaps
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 22851
LENGTH: 201
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          DB 7; Length 201;
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                                                       30; Indels
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     20.1%; Score 31; DB 7; 62.0%; Pred. No. 0.51; tive 0; Mismatches
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GENERAL INFORMATION:
THEORY: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: STENOSIS, METHODS OF DET
FILE REFERENCE: CLOO1524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT APPLICATION NUMBER: US/60/568,845
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22554
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                              183 GACTACTGAGTTGGAAGAT 201
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Query Match
Best Local Similarity 62.09
Matches 49; Conservative
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Best Local Similarity 62.0
Matches 49; Conservative
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Matches 49; Conservative
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; ORGANISM: Homo sapiens
US-60-568-845-22851
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; ORGANISM: Homo sapiens
US-60-568-845-22854
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Local Similarity 63.9
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                                                                                                                                                                                                           ORGANISM: Homo sapiens
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US-60-568-845-22832
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82 AAGGAAGGAAGGAAGGAAGAAGAAAAAAAAAGAGAAAACAGAAACATTGCAACAAT 141
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT PILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22858
LENGTH: 201
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.ahes 30; Indels
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                                                                                                                                                                                              APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS;
TITLE OF INVENTION: STENOSIS, METHODS OF DE:
FILE REFRENCE: CL001524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22856
                                                                                                                                                                Sequence 22856, Application US/60568845 GENERAL INFORMATION:
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                                                                       142 GACTACTGAGTTGGAAGAT 160
                                     113 GTCTTCCCAGCTCACAAAT 131
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49; Conservative
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Best Local Similarity 62.0%
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(96902)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-2 US-60-568-845-2915
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOLIS4
CURRENT APPLICATION NUMBER: US/60/569,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39604
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 22832
LENGTH: 2014
                                                               DETECTION AND USES THEREOF
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US-60-568-845-22842
US-60-568-845-22842, Application US/60568845
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001524
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENSIS, METHODS OF DETECTION AND US
FILE REFERENCE: CLOO1524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FASEUSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7;
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20.1%; Score 31; DB 7
Best Local Similarity 62.0%; Pred. No. 6.4;
Matches 49; Conservative 0; Mismatches
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CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
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GENERAL INFORMATION:

APPLICANT: MAI GENOMICS, INC.

APPLICANT: DAVISE, SUE K.

APPLICANT: DAVISE, SUE K.

APPLICANT: BATES, SUE K.

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

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APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, DAVID

CURRENT APPLICATION NUMBER: PCT/US03/41761

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PALENTIN VERSION 3.1

ENGTH: 1207
                                                                                                                                                                                                                372 GCCATGGAAAACTGCCAGAIGGTAATGAATTTTAGCCACTGCTGACTTCAGCTGGATAC 313
                                                                                                                                                                                                                                                                      69 AATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACA 128
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                                                                                                                                                               312 AAACAAATGACCTAAGGAGACAGATTCCATATCTTACTTCTAATCCCTTCAAGCTAACA
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOG1524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FASLSEQ for Windows Version 4.0
LENGTH: 201
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                                                           Query Match 19.7%; Score 30.4; DB 1; Length 1207; Best Local Similarity 53.3%; Pred. No. 1.7; Matches 64; Conservative 0; Mismatches 56; Indels 0
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Best Local Similarity 53.3%; Pred. No. 1.7;
Matches 64; Conservative 0; Mismatches 56; Indels 0
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PCT-US03-41761-31797/c
· Secuence 31797, Application PC/TUS0341761
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; Sequence 22830, Application US/60568845
; GENERAL INFORMATION:
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PCT-US03-41761-31797
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; ORGANISM: Homo sapiens
US-60-568-845-22830
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Best Local Similarity
Matches 45; Conserv
          PCT-US03-41761-31797
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| Sequence 31797, Application PC/TUS0341761
| Sequence 31797, Application PC/TUS0341761
| Sequence 31797, Application PC/TUS0341761
| APPLICANT: NAI GENOMICS, INC. |
| APPLICANT: CHARTERIS, Paul |
| APPLICANT: HOLM, Tom |
| APPLICANT: HOLM, Tom |
| APPLICANT: HOLM, Tom |
| APPLICANT: BATES, Stephen |
| TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING BOVINE BREED |
| FILE REFERENCE: MAILISOWO |
| CURRENT APPLICATION NUMBER: DCT/US03/41761 |
| CURRENT FILING DATE: 2003-12-31 |
| PRIOR PLIING DATE: 2003-12-31 |
| NUMBER OF SEQ ID NOS: 64922 |
| SOFTWARE PAPELICATION VERSION 3.1
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 204-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FASTSEQ for Windows Version 4.0
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Pred. No. 0.83;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 22842
LENGTH: 201
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l Similarity 63.9%;
46; Conservative
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Matches 46; Conservative
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US-60-568-845-22842
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; ORGANISM: Homo sapiens
US-60-568-845-22845
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Best Local Similarity
Matches 46; Conserv
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US-60-568-845-22845
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LENGTH: 1207
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Search completed: May 18, 2004, 20:26:20 Job time: 71.55 secs

Sequence:

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Database

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CD833983 BN45.0400
CD827413 BN25.067G
CD834406 BN45.040H
CD834592 BN40.0630
CD834904 BN45.040E
CD834994 BN45.040E
CD834994 BN45.040E
CD834994 BN45.040E
CD834994 BN45.040E
CD8313779 BN45.040I
CD837517 BN45.051
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CD831294 BN40.058M
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CC883756 SALK_0960
Z29957 ATTS2387 PE
Z27258 ATTS2387 PE
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BN40.064A14F011227 BN40 Brassica napus cDNA clone BN40064A14, mRNA
Sequence.
CD832625.
EST.
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BG331515 Ds01 08a0
CA992140 HCO577 GI
CD831226 BM40.0584
CD83784 BM45.0011
CD834095 BM45.0011
CD834095 BM45.0401
CD833924 BM45.0401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoplante, a major partnership french program in plant genomics Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93, fur Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                           CD831972
CD834068
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Brassica napus
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KEYWORDS
SOURCE
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TITLE
JOURNAL
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CD832625
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CD834168 BN45.040N
CD833944 BN45.040B
CD826491 BN25.064A
                                                                                   May 18, 2004, 17:05:11; Search time 1282.4 Seconds (without alignments) 3586.070 Million cell updates/sec
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
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Maximum DB seq
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CD833944 420 bp mRNA linear EST 10-UUL-2003
BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
sequence.
CD833944.1 GI:32515884
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BN25.064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, mRNA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

    (Dases 1 to 421)

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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93, rue Fenri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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B7.6%; Pred. No. 6.2e-27;
ive 0; Mismatches 19; Indels
                                     154
                                                      260 GCTCACAAGTGTATTTGCTACTTCCCTTGTTAA 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Brassica napus"
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/clone="RNA5040B07"
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/clone_lib="BN45"
                             122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA
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CD826491.1 GI:32508431
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Brassica napus
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Genoplante
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419 bp mRNA linear EST 10-JUL-2003
BN45.040N06F011018 BN45 Brassica napus cDNA clone BN45040N06, mRNA
                                                                                                                                                                                                                                                                                              62 AGGRACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
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                                                                                                                                                                          Query Match 79.6%; Score 122.6; DB 14; Length Best Local Similarity 87.6%; Pred. No. 6.2e-27; Matches 134; Conservative 0; Mismatches 19; Indels
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                            263 GCTCACAAGTGTATTTGCTACTTCCCTTGTTAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                     122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA
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CD833977 421 bp mRNA linear EST 10-JUL-2003
BN45.040D05F011019 BN45 Brassica napus CDNA clone BN45040D05, mRNA
sequence.
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(bases 1 to 421)
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Contact: Genoplante
Genoplante
                                                                                                                                       2 AGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGITIGIGGGAACAACAAIGCAIGC
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                                                          DB 14; Length 421;
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                                                      Score 122.6; DB 14;
Pred. No. 6.2e-27;
0; Mismatches 19;
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                                                      Query Match 79.6%;
Best Local Similarity 87.6%;
Matches 134; Conservative
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                                                                                                      93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00

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This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

Location/Qualifiers
                        Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
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Tel: 33 1 69 47 54 00
Tel: 33 1 69 47 54 10
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79.6%; Score 122.6; DB 14; Length 421;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0;
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CD831111.1 GI:32513051
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Brassica napus
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CD831111
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UD42/413
BN25.067G02F020123 BN25 Brassica napus CDNA clone BN25067G02, mRNA
Bequence.
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    (bases 1 to 426)

        Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93, rue Henri Rochefort 91025 EVRY CEDEX France
191: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infoblogen.fr).
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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
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                                                                                                          1. .422
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/cultivar="Jet neuf"
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CD827413.1 GI:32509353
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Brassica napus
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Best Local Similarity 87.6'
Matches 134; Conservative
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Best Local Similarity
Matches 134; Conserv
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CD827413
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                  CD831972 422 bp mRNA linear EST 10-JUL-2003 BN40.061108F011228 BN40 Brassica napus cDNA clone BN40061108, mRNA
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BN45.040D11F011019 BN45 Brassica napus CDNA clone BN45040D11, mRNA
sequence.
                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                  93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Tel: 33 1 69 47 54 00
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Pred. No. 6.2e-27;
0; Mismatches 19
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CD831972.1 GI:32513912
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CD833983.1 GI:32515923
                                                                                                                                    Brassica napus (rape)
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Best Local Similarity 87.6%;
Matches 134; Conservative
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CD833983
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Brassica napus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rOsids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 446)
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Brassica napus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Iosids, eurosids II; Brassicales; Brassicaceae; Brassica.
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Contact: Genoplante
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Tel: 33 1 69 47 54 00
Tel: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
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Contact: Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Brassica napus"
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                Brassica napus (rape)
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CD832592
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BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA sequence.
CD834068
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                                                          62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAAACTGCAACTATGTCTTCCCA 121
                                                                                  Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Contact: Genoplante
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79.6%; Score 122.6; DB 14; Length 438;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0;
                                                                                                                                                             261 GCTCACAAGTGTATTTGCTACTTCCCTTGTTAA 293
                                                                                                                                         122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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CD831479.1 GI:32513419
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FEATURES

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/organism="Brassica napus"

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19;

DB 14; Length 446; Indels

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cuds#UUB
BN45.040E18F011019 BN45 Brassica napus CDNA clone BN45040E18, mRNA
sequence.
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BN45.043006F011229 BN45 Brassica napus cDNA clone BN45043006, mRNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Tel: 35 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                                                                                                                                   Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
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Brassica napus
Brassica napus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo|
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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         122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                             280 GCTCACAAGIGTATTTGCTACTTCCCTTGTTAA 312
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Pred. No. 6.3e-27;
0; Mismatches 19
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Matches 134; Conservative (
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BN40.061003F011227 BN40 Brassica napus cDNA clone BN40061003, mRNA
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pepmratophyta, Magnoliophyta, eudicotyledons; core eudicots;
roaids, eurosids II; Brassicales, Brassicaceae, Brassica.
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Genoplante.
Genoplante, a major partnership french program in plant genomics
Uppublished (2003)
Contact: Genoplante
Genoplante
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Location/Qualifiers
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Pred. No. 6.3e-27;
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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93. The Henri Rochefort 91025 EVRY CEDEX France
13. 169 47 54 00
Fax: 33 169 47 54 00
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

1. 458
| Location/Qualifiers |
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Contact: Genoplante
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79.6%; Score 122.6; DB 14; Length 458;
Best Local Similarity 87.6%; Pred. No. 6.3e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0;
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Search completed: May 18, 2004, 19:00:30 Job time: 1283.4 secs

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RESULT 1
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                                                                                                    May 18, 2004, 19:02:23 ; Search time 2171 Seconds (without alignments) 998.227 Million cell updates/sec
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1 RLCERPSGTWSGVCGNNNAC......EHGSCNYVFPAHKCICYFPC 50
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                       OM protein - nucleic search, using frame_plus_p2n model
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30: em_htg_hum:*
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39: em_htgo_hum:*
40: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Cy         1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAsnAlaCys         20           Db         109 AGSTIGFGGGAGAGACAAGTGGGGGGGAGGGAGCACCACGACGGGGGGGAGCACCACGACG	ACTURE ALTURE TO THE TO	Alignment Scores:     3.61e-27	Qy         1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys 20           Db         117 AGGTGGGAGAGACCAAGTGGGACATGGTCAGGATTTGTGGGAACAATGCTTGC         176           Qy         21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40         177 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 236           Qy         41 AlaHisLysCysIleCysTyrPheProCys 50           Db         222 Alamanamamamamamamamamamamamamamamamamama	SULT 4 432389 AR CUS CUS CUS CUS CUS CUS CUS CUS CUS CUS	SOURCE OURGANISM Unknown.  ORGANISM Unclassified.  ERFERENCE I (bases 1 to 286)  AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.  TITLE Antifungal polypebtide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi JOURNAL Patent: US 652180-A 12 25-NOV-2003;  FEATURES Location/Qualifiers  Source /organism="unknown"
LOCUS LOCUS DEFINITION Sequence 14 from patent US 5773696. ACCESSION AR014691.1 GI:3972145 VERNORDS SOURCE ORGANISM Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unclassified. Unknown. Unclassified. Uncl	Alignment Scores:  Pred. No.:  Socre:	21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValbhePro 40	1 ION ON S S ISM CE	Title Antitungal polypeptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi JOURNAL Patent: US 6653280-A 14 25-NOV-2003, FEATURES Location/Qualifiers 1. 270 / Organism="unknown" / Mol_type="genomic DNA"	Alignment Scores:     3.38e-27

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Unknown.
Unclassified.
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1 (base 1 to 285)
Liang, J., Shah, D.Maganlal., Wu, Y.Shun. and Rosenberger, C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
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                                                Unclassified.

1 (bases 1 to 500)

Liang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.
Antifungal polypeptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi
Patent: US 6653280-A 9 25-NOV-2003;

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Sequence 16 from patent US 5773696.
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Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic fungi.
Us 5773696-A 9 30-JUN-1998,
Location/Qualifiers
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 Direct Submission
Submitted (14-DBC-1994) Franky R. Terras, F.A. Janssens Laboratory
of Genetics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-300,
On Feb 9, 1995 this sequence version replaced gi:609321.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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1. 395
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15. 257
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'note="18 A nucleotides"
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/citation=[1]
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                             181 AAGAACCAATGCATCAACCTCGAGAAGGCACGGCATGGATCTTGCAACTACGTCTTCCCA 240
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1 (bloom, R. G., Eggermont, K., Kovaleva, V., Raikhel, N.V.,
1 Osborn, R.W., Kester, A., Rees, S.B., Torrekens, S., Van Leuven, F.,
1 Vanderleyden, J., Cammue, B.P.A. and Broekaert, W.F.
1 Small cysteine-rich antifungal proteins from radish: their role in
1 host defense
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosida, eurosida II, Brassicales, Brassicaceae, Raphanus.
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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
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1 (Dases 1 to 285)

Lidang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.

Antifungal polypeptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi
Patent: US 6652380-A 16 25-NOV-2003;

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Sequence 16 from patent US 6653280.
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2 (bases I to 395)
Terras, F.R.
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PAT 30-NCV-2001

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

JOURNAL REFERENCE AUTHORS

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/db_xref="taxon:32644"
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                                                                                                                                         A63404 414 bp Sequence 19 from Patent WO9721814.
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/mol_type="unassigned DNA"
                                                              41 AlaHisLysCysIleCysTyrPheProCys
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A63404.1 GI:3717176
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AR050153
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           Osborn, R.W. and Rees, S.B. BIOCIDAL PROTEINS PROJECT NO 9305153-A 33 18-MAR-1993; ICI PLC (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unidentified
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bubock,A.C., Powell,K.A. and Rees,S.B.
ANTINICROBIAL-PROTBIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
EARERT: WO 9416076-A 37 21-JUL-1994;
  eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicorosida; eurosida II; Brassicales; Brassicaceae; Raphanus. (Dases 1 to 414)
Broekaert, W.F., Cammue, B.P.A., Terras, F.R.G., Vanderleyde.
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Location/Qualifiers
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Sequence 37 from Patent W09416076.
A39549
A39549.1 GI:2295842
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PAT 29-SEP-1999
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Patent: WO 9721814-A 19 19-JUN-1997;
ZENECA LTD (GB)
Other publication AU 1105397 19970703.
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                                                                                                       Unclassified.

1 (bases 1 to 414)
Brockaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
Blocidal proteins
Patent: US 6187904-A 48 13-FEB-2001;
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                                                                                                                                                                                                                             AR130272 414 bp
Sequence 48 from patent US 6187904.
AR130272.1 GI:14118169
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AR130272
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Arabidops A. thalia Rs-AFP2 c Antimicro

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Aaq38652 | Aaq70130 | Aaa53190 | Aaz99324 |

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Aaz51396 Aaz99327 Aaz99327 Aaz99326 Aaz99326 Abz1941 Abz192136 Abz1933 Abz19332 Aaz99333 Aaz99333 Aaz99333 Aaz99333 Aaz99333 Aaz99333 Aaz99333 Aaz99333 Aaz99333 Aaz99333

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Amplified Alyssum species antifungal polypeptide gene from pMON22652.
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AAQ70129
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AAZ99331
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AAZ99333
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       ADC51223
ADA68378
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                      AAV10632
                                            AAA53190
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22. .261
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                                                                                                                                                                                                                                                                                                                                    AAT94582 standard; DNA; 270
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27-MAR-1997;
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AAT94582;
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Aat94582 Amplified
Aat94574 Alyssum s
Aat9289 Alyssum s
Aat94581 Composite
Ad51221 Brassica
Aag36650 Rs-AFPI c
Aag70128 Antimicro
Aat70233 Raphanus
                                                    May 18, 2004, 19:00:43; Search time 299 Seconds (without alignments) 710.401 Million cell updates/sec
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                                                                                           305

1 RLCERPSGTWSGVCGNNNAC......EHGSCNYVFPAHKCICYFPC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                      - nucleic search, using frame_plus_p2n model
                                                                                                                                                                              of hits satisfying chosen parameters:
                                                                                                                                                               3373863 seqs, 2124099041 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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AAT94574
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                                                                                                     This sequence represents the cDNA sequence cloned into the E. coli cassette vector pMON2317 to generate vector pMON22652. The cDNA encodes the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum. The AlyAFP polypeptide can be used to control phytopathogenic tungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                                                                                                  168
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                                                                                                                                                                                                                                                                                             109 AGGITGIGGGAGAGACCAAGIGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATGC
                                                                                                                                                                                                                                                                                                                 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                             /*tag= a
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                                                             Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi
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117. .269
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                                                                                         Example 4; Page 69; 92pp; English.
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                                                  P-PSDB; AAW35560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rungı, whilst the DNA can be used to produce transgenic plants that express the protein making them resistant to the phytopathogenic fungi
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                                                                                                                          Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "AlyAFP antifungal polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 286 BP; 80 A; 62 C; 65 G; 79 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
53. .292
/*tag= a
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                                                                                                                                                                                        Claim 12; Page 68; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1,13e-26
305.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a //product= '/product= '/*tag= b //*tag= b //*tag= c //*tag= c 439. .443
                                    Wu Y,
                                                                          WPI; 1997-503109/46.
P-PSDB; AAW35558.
(MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                      Shah D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT99289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
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WO9737024-A2

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Liang J,
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                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the cDNA sequence which encodes the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum. The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                            ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                         1 ArgieuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                               Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composite cDNA sequence for Alyssum species antifungal polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antifungal polypeptide; AlyAFP; inhibition; transgenic plant; phytopathogenic fungus; resistance; ss.
                                                                                                                                                                                                         Sequence 481 BP; 147 A; 88 C; 91 G; 154 T; 0 U; 1 Other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                         Rosenberger CA;
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                                                                                                                                        Example 4; Fig 1; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                            AAT94581 standard; DNA; 500 BP
                        97WO-US005709
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                                        96US-00627706
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100.00%
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                                                                         Wu Y,
                                                                                       WPI; 1997-503109/46.
P-PSDB; AAW35560.
                                                                       Shah D,
                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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                                                        (MONS ) MONSANTO
                       27-MAR-1997;
                                        29-MAR-1996;
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Pred. No.:
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      09-OCT-1997
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                                                                         Liang J,
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DB:
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This sequence represents the cDNA sequence encoding the antifungal polypeptide AlyAFP, from plants of the genus Alyssum. The sequence represents a composite of the sequences isolated by 5' and 3' RACE (Rapid Amplification of cDNA Ends) methods (see AAF94577) and AAF94580). The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                       Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi.
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/product= "Brassica oleracea defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       composite disease resistance; pathogenic bacteria; rice white leaf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica oleracea defensin protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antimicrobial protein; defensin; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
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  Rosenberger CA;
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                                                                                                                                                                                      Example 4; Page 67; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC51221 standard; DNA; 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5e-25
296.00
98.00%
96.00%
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Wu Y,
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                                                     WPI; 1997-503109/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Shah D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica oleracea.
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91 AAGTTGTGCGAGAGGCCAAGTGGGACTCTGGGAGTCTGGGAAACAATAACGCATGC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamencous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                       The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPheFro
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                                                                              G; 125 T; 0 U; 0 Other;
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4 0 0 0
                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
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16. .256
/*tag= a
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                                                                                                                         Claim 3; SEQ ID NO 1; 34pp; Japanese
                                                                                                                                                                                                                                                                                 Sequence 394 BP; 116 A; 71 C; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ38650 standard; DNA; 414 BP
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283.00
96.00%
90.00%
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                             WPI; 2003-621123/59.
P-PSDB; ADC51222.
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Best Local Similarity:
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Pred. No.:
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This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for primer AAQ38640 was used together with AAQ38641 to generate a probe for common acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp coduct was partially re-amplified using AAQ38642 and AAQ38641 to give a product, which was further reamplified with the same primers and 123bp product, which was used to GTTP to give a digoxigenin-11-dUTP instead of GTTP to give a digoxigenin labeled PCR cigoxigenin-11-dUTP instead of GTTP to give a digoxigenin labeled PCR compared by pridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of halper phage their size compared by agarose gel electrophoresis. Four clones had inserts of insert sizes of approx. 400bp the others between 250-300bp. The inserts compared by agarose gel electrophoresis. Four clones had compared and found to differ only in the length of their S' and 3' UTR's. The longest sequence is given here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225
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                                                                                                                                             Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAsnAlaCys
                                                                        Terras FRG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
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Mismatches:
                                                                        Rees SB,
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                                                                        Cammue BPA, Osborn RW,
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                                                                                                                                                                                                              Example 21; Fig 35; 110pp; English.
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                                             (ICIL ) IMPERIAL CHEM IND PLC
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283.00
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90.00%
92GB-00003038.
92GB-00013526.
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                                                                                                                       WPI; 1993-100978/12.
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                                                                                           Vanderleyden J;
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                                                                             Broekaert WF,
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   13-FEB-1992;
25-JUN-1992;
                                                                                                                                                                                       diseases.
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DB:
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Raphanus sativus

Van Amerongen A;

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166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                    Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA sequence encodes an Rhapanus sativus (radish) antifungal protein (Rs-AFP1). Analogues of the homologous protein, Rs-AFP2 (AAM19281), have also been produced (see AAM19282-92, AAM1928-94, AAM19281). Have also been produced (see AAM19282-92, AAM1928-94, AAM1930-104, AAM1930-134, and AAM31765-834). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease tolerance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ArgleucysGluargProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                  Sijtsma L, Van Amerong
Borremans FAM, Rees SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                  /product= "antifungal_protein_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCACAAGIGTATCTGCTACTTTCCTTGT 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-681-972-2 (1-50) x AAT72333 (1-414)
                                                                                                                                                                                                                                                                                                  iijk WC, Schaaper WMM,
Samblanx GW, Fant F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT68696 standard; cDNA; 414 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Fig 2; 65pp; English.
                                                                                                                                                                                                           95GB-00025455.
                                                                                                                                                                           96WO-GB003068
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96.00%
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ag= b
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                                                                                                                                                                                                                                                                (ZENE ) ZENECA LID.
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                                                                                                                                                                                                                                                                                                   Puijk
                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW19280.
                                                                                                                                                                                                                                                                                                                    Broekaert W, Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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                                                                                                                                                                               12-DEC-1996;
                                                                                                                                                                                                                13-DEC-1995;
                                                                                                                                                                                                                                   28-MAR-1996;
                                                                                                         WO9721815-A2
                                                                                                                                            19-JUN-1997
 sig_peptide
                                   mat_peptide
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antifungal protein; candida; fungal resistance; food additive; radish; crop protection; plant defensin; bacterial protection; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                            plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA sequence of Rs-AFP1 is given in AAQ70128. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                        Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 AGTICICCAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
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/transl_except= (pos:85. .87, aa:Glu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raphanus sativus antifungal protein I (Rs-AFPI) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaHisLysCysileCysTyrPheProCys 50
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 31; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT72333 standard; cDNA; 414 BP
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283.00
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90.00%
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                                                                                                                                                                                                           Powell KA,
                                                                                                                                                                                                                                            WPI; 1994-249223/30.
                                                                                                                                                                          (ZENE ) ZENECA LID
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Best Local Similarity:
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                                                                                                                                                                                                                                                                  P-PSDB; AAR57325
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Pred. No.:
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19-JAN-1998
                                                                                                   05-JAN-1994;
                                                                                                                                        08-JAN-1993;
                                 WO9416076-A1
                                                                  21-JUL-1994
                                                                                                                                                                                                              Dubock AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47
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RESULT

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ADC51223

.87, aa:Glu)

(pos:85.

Location/Qualifiers
16. .258
4/transl except= (pos. 16. .102
6/trag= b/(103. .255
/\*tag= c

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This cDNA clone codes for the preprotein for radish antifungal protein 1 (Rs-AFP1) (AAW19617). Novel antifungal proteins are based on Rs-AFP1, Rs-AFP2 (see AAW19616), Rs-AFP3 and Rs-AFP4, especially those in which Gly9 is repaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly9 Met. Mutants (see AAW26371-90) of Rs-AFP2 are specifically claimed. The mutants show improved salt tolerant antifungal activity, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 AAGTIGIGGAAAGGCCAAGTGGGACAIGGICAGGAGTCTGIGGAAACAAIAACGCAIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.
                                                                     Rs-AFP1; radish antifungal protein 1; fungicide; salt tolerance; preservative; transgenic plant; crop protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaHisLysCysIleCysTyrPheProCys 50
                                                Radish antifungal protein 1 (Rs-AFP1) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-681-972-2 (1-50) x AAT68696 (1-414)
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                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                             (ZENE ) ZENECA LTD.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW19617.
                                                                                                                Raphanus sativus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                            12-DEC-1996;
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                                                                                                                                                                                                                                                           WO9721814-A1
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                        13-DEC-1997
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Query Match:
DB:
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SB; Rees

De Samblanx GW,

96WO-GB003065 95GB-00025474

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Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 AAGTTGTGCGAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                    composite disease resistance, pathogenic bacteria;
rice white leaf blight, brown-stripe disease, glume blight;
seedling damping-off disease; filamentous fungi; rice blight;
sheath blight disease, leaf blight; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "Brassica defensin protein"
                                                                                                                     protein; defensin; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                         Brassica defensin protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 AlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; SEQ ID NO 3; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-681-972-2 (1-50) x ADC51223 (1-426)
                                                                                                                                                                                                                                           Location/Qualifiers
BP.
                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-2001; 2001JP-00283117.
                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-2001; 2001JP-00283117
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283.00
96.00%
90.00%
 standard; DNA; 426
                                                            (first entry)
                                                                                                                                                                                                                                                        .243
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P-PSDB; ADC51224.
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                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
                                                            18-DEC-2003
                                                                                                                                                                                                                Brassica sp.
                               ADC51223;
 ADC51223
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165

226

RESULT 10

44 % % C O O O

Length:
Matches:
Conservative:
Mismatches:
Indels:

.46e-24 283.00 96.00% 90.00% 92.79% 210

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Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes the Arabidopsis PDF1.1 gene which is used in a novel method for the protection of plants against pathogens which involves inducting expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ArgieuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manners
                                                                                                                          Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Terras FRG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                 /product= "PDF1.1"
/note= "plant defensin"
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                                                                                                                                                                                         Location/Qualifiers
26. .268
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                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thomma BPHJ,
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                       AAV10632 standard; DNA; 403
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96.00%
88.00%
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114. .265
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                                                                                                                                                                 Arabidopsis thaliana
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Best Local Similarity:
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                                                                                                                                                                                                                                 sig_peptide
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                                                                         23-JUN-1998
                                                                                                   A. thaliana
                                                                                                                                                                                                                                                          mat_peptide
                                                                                                                                          fungi; ss
                                                AAV10632
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No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150
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                                                                                                                                                                                                                                                                                                                                                                                                     Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                                                      Plant; bacterial infection; fungal infection; viral infection; ds.
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                                                                                                                                                                                                                                                                                                                                      Glazebrook J, Goff SA,
Whitham S, Xie Z, Zhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
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Mismatches:
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GCTCACAAGTGTATTTGCTACTTCCCTTGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; SEQ ID NO 747; 899pp; English.
                                                                                                                               SEQ ID 747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-681-972-2 (1-50) x ADA68378 (1-243)
                                                                                                                                                                                                                                                                                                           (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                    BP.
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                                                                                                                                                                                                                                                                                      22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                             22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28e-23
                                                    243
                                                                                                                                Arabidopsis thaliana gene,
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96.00%
88.00%
91.15%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
                                                   ADA68378 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                    Katagiri F, Quan S,
                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-175290/17.
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                                                                                                                                                                                                            WO2003000898-A1.
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                                                                              ADA68378;
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Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial
                                                                                                        Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                                                                     Cammue BPA, Osborn RW, Rees SB,
Location/Qualifiers
16. .256
/*tag= a
                                           BP
                                                                                                                                                                                                                            91GB-00018523.
92GB-00003038.
92GB-00013526.
                                                                                                                                                                                                                                                        (ICIL ) IMPERIAL CHEM IND PLC
                                                                                                                                                                                                              92WO-GB001570.
                                          AAQ38652 standard; DNA; 261
                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                            WPI; 1993-100978/12
                                                                                                                                        Raphanus sativus.
                                                                                                                                                                                                                                                                       Broekaert WF, 'Vanderleyden J;
                                                                                                                                                                                                                             29-AUG-1991;
13-FEB-1992;
                                                                                              RB-AFP2 CDNA.
                                                                                                                                                                                                               27-AUG-1992;
                                                                                                                                                                                                                                           25-JUN-1992;
                                                                                                                                                                                    WO9305153-A1
                                                                        25-MAR-2003
07-JUL-1993
                                                                                                                                                                                                 18-MAR-1993
                                                                                                                                                                                                                                                                                                                          diseases.
                                                         AAQ38652;
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Example 21; Fig 35; 110pp; English.

This cDNA represents the sequence of Rs-AFP2 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 133bp product. Which was further reamplified with the same primers and digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ product. This was used to screen a lambda ZAPII cDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two plaque hybridisation positive plaques were excised by RcoRI digestion and vivo into the pBluescript phagemid form with the aid of halper phage cribers is zec compared by agarose gel electrophoresis. Four clones had contained to their accordance and found to differ only in the largest captence was identified as Rs-AFP1 so the Rs-AFP2 was seen to differ by only 2 amino acids from Rs-AFP1, so the Rs-AFP2 was seen to differ by only 2 amino acids from Rs-AFP1, so the Rs-AFP2 was seen to differ mutagenesis. (Updated mutagenesis. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;

Alignment Scores:

Plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFPI form. sativus. The full-length cDNA sequence of PCR assisted site-directed mutagenesis of Rs-AFP2 is given in AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-Antimicrobial; Rs-AFP2; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; PCR; polymerase chain reaction; mutagenesis; ss. Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease. 1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys G; 83 T; 0 U; 0 Other 288 43 4 261 443 00 00 Length: Matches: Conservative: Length: Matches: Conservative: Mismatches: Indels: 41 AlaHisLysCysIleCysTyrPheProCys Gaps: US-10-681-972-2 (1-50) x AAQ38652 (1-261) Disclosure; Page 33; 39pp; English. 70 A; 66 C; 69 BP. MAR-2003 to correct PN field.) 93GB-00000281. Rees 94WO-GB000012 4.61e-23 274.00 94.00% AAQ70130 standard; cDNA; 288 4.08e-23 (first entry) 274.00 94.00% 86.00% 89.84% Dubock AC, Powell KA, (revised) Antimicrobial Rs-AFP2 WPI; 1994-249223/30. (ZENE ) ZENECA LTD. Sequence 288 BP; Percent Similarity: Best Local Similarity: Raphanus sativus. P-PSDB; AAR57327 Score: Percent Similarity: WO9416076-A1. Alignment Scores: 05-JAN-1994; 08-JAN-1993; 21-JUL-1994. 25-MAR-2003 14-FEB-1995 AAQ70130; Query Match: Pred. No.: RESULT 14 AAQ70130 Score: 셤 à à g à

Terras FRG;

Mismatches:

Indels:

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Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance of rice paddy against pathogenic microbes.
                                                                                                          1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAsnAlaCys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes an antibacterial protein, designated radishin, isolated from Raphanus sativus (radish). A phage or plasmid comprising radishin can be used for increasing resistance of paddy and rice blast disease against pathogenic microbes
                                                                                                                                                                                                                                                                                                        Raphanus sativus; antibacterial; plant; resistance; paddy; radishin; pathogenic microbe; radish; rice blast disease; ds.
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                                           US-10-681-972-2 (1-50) x AAQ70130 (1-288)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 4; 7pp; Japanese.
                                                                                                                                                                                                                        BP.
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P-PSDB; AAY91117.
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Best Local Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2000.
                                                                                                                                                                                                                                              AAA53190;
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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
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US-08-627-706-14

Sequence 14, Application US/08627706

Patent No. 5773696

PAPELICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 63198

CMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
US-08-377-687-48

US-08-77-192-48

US-08-77-982-48

US-09-077-981-19

US-09-077-948A-45

US-09-077-948A-45

US-09-103-489-17

US-08-377-192-58

US-08-377-192-58

US-08-377-192-58

US-08-377-192-58

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US-08-971-982-36
US-09-589-733C-6
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US-08-377-687-34
US-08-777-192-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (314)537-6047
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO spool/US10681972/runat_17052004_151740_4379/app_query.fasta_1.199
-Q=/cgn2_1/USPTO spool/US10681972/runat_17052004_151740_4379/app_query.fasta_1.199
-DB=ISSUGA_PATENTE NA -OFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LCOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE_LOCAL -OUTFRT=pto -NOFM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10681972_@CGN_1 1 -44 @runat_17052004_151740_4379 -NCPU=6 -ICFU=3
-NOO_MMAP -LARGEQÜBRY -NEG_SCORES=0 -MATT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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440.437 Million cell updates/sec
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                         - nucleic search, using frame plus p2n model
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Listing first 45 summaries
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Reacherger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: 20
CORRESPONDENCE ADDRESS: 20
CORRESPONDENCE ADDRESS: ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STARET: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER: IBA PC Compatible
COMPUTER: IBA PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UN-1998
CLASSIFICATION NUMBER: 34,565
REGIENATION NUMBER: 34,565
REFERENCE CORACET NUMBER: 38-21 (10700) A
TELEFANY: (314) 537-624
TELECOMMUNICATION INFORMATION:
TELEFANY: (314) 537-624
TELEFANY: (314) 537-624
TELEFANY: (314) 537-624
TELEFANY: CHARLETISTICS:
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US-09-103-489-14
; Sequence 14, Application US/09103489
; Patent No. 6215048
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-627-706-14
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US-09-829-381D-14

| Sequence 14, Application US/09829381D |
| Sequence 14, Application US/09829381D |
| Sequence 14, Application US/09829381D |
| Patent No. 6553280 |
| GENERAL INFORMATION: |
| APPLICANT: Liang, Jihong |
| APPLICANT: Shah, Dilip M. |
| APPLICANT: Rosenberger, Cindy A. |
| TITLE OF INVENTION: Plant Pathogenic Fungi |
| TITLE OF INVENTION: Plant Pathogenic Fungi |
| TITLE OF INVENTION: Plant Pathogenic Fungi |
| TITLE OF INVENTION: Plant Pathogenic Fungi |
| TITLE OF INVENTION: Plant Pathogenic Fungi |
| TITLE OF INVENTION: Plant Pathogenic Fungi |
| TITLE OF INVENTION: Plant Pathogenic Fungi |
| FILE REPERENCE: 38-21 (10700) C |
| CURRENT FILING DATE: 2001-04-09 |
| PRIOR FILING DATE: 1998-06-24 |
| NUMBER OF SEQ ID NOS: 20 |
| SEQ.ID NO 14 |
| LEAST FUNGINE OF SEQ ID NOS: 20 |
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, OTHER INFORMATION: Plasmid
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
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US-09-103-489-12
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                                                         APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
                                                                                                                                                                                                                                                                                                                             ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
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Matches:
Conservative:
Mismatches:
Indels:
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; Sequence 12, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Rosenberger, Cindy A.
Sequence 12, Application US/08627706
Patent No. 5773696
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 436
ATTORNEY AGENT INFORMATION:
NAME: COhen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
INFORMATION FOR SEQ 1D NO: 12:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Missouri
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Sequence 12, Application US/09829381D

Sequence 12, Application US/09829381D

BEENT No. 655280

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Younie S.

APPLICANT: Rosenberger, Cindy A.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control

TITLE OF INVENTION: Plant Pathogenic Fungi

FILE REFERENCE: 38-21 (10700) C

CURRENT APPLICANION NUMBER: US/09/829,381D

CURRENT FILING DATE: 2001-04-09

PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176
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Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
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TITLE OF INVENTION: Antifungal Polypeptide and Methods for ITILE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F SIREET: 700 Chesterfield Village Parkway No. 6215048th CITY: St. Louis STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: US/09/103,489
FILING DATE: US/09/103,489
FILING DATE: US/09/103,489
FILING DATE: US/08/103,489
FILING DATE: US/08/103,489
FILING NATE: COCHOIN NUMBER: 34,565
REGISTRATION NUMBER: 34,565
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STREET: 700 Chest
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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Query Match:
MOLECULE TYPE:
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| Sequence 9, Application US/08627706
| Patent No. 5773696
| GENERAL INFORMATION:
| APPLICANT: Itang, Jihong
| APPLICANT: Shah, Dilip M.
| APPLICANT: Ru, Yonnie S.
| APPLICANT: Ru, Yonnie S.
| APPLICANT: Ru, Yonnie S.
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MEDIUM TYPE: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLAN FC. COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic PCR reaction product US-09-829-381D-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-681-972-2 (1-50) x US-09-829-381D-12 (1-286)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REPERENCE/DOCKET NUMBER: 38-21 (10700) A
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: (314)537-624
TELEPRAX: (314)537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: mucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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305.00
100.00%
100.00%
          NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 286
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CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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Best Local Similarity:
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DB:
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US-08-627-706-9

Alignment Scores:

Accine No. 200-29 Macches: 500

Beccan Smilarity: 98-004 Conservative: 1

Deery Match: 97.054 Index. 1

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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
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APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Attifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                              3: Charles E. Cohen, Monsanto Company, BB4F 700 Chesterfield Village Parkway No. 5773696th
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Wu, Yonnie S.
APPLICANT: Wu, Younie S.
TITLE OF INVENTION: Antifungal Polypeptide and Methods JITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDEMES: Charles E. Cohen, Monsanto Company, BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER 1984

COMPUTER READABLE FORM:

MEDITUM TYPE: Eloppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/627,706

FILING DATE:

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: COhen, Charles E.

REPREMENCE/POCKET NUMBER: 38-21(10700)A

TELETHONE: (314/537-6424

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Matches:
Conservative:
Mismatches:
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DESCRIPTION: /desc = "synthetic DNA"
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Patent No. 6215048
GENERAL INFORMATION:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                     STREET: 700 Ches CITY: St. Louis STATE: Missouri
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Patent No. 6653280

GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Clidy A.
ITILE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Dilip M. Yamide S.
TITLE OF INVENTION: Plant Pathogenic Fungi,
TITLE OF INVENTION: Dilip M. Yamide S.
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                                                                                                                                                                                                                                                                                 159 AAGTTGTGCGAGAGTCCAAGTGGAACATGGTCAGGCGTGTGTGGGGAATAATAACGCATGC 218
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Matches:
Conservative:
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Indels:
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LOCATION: (22)...(22)
OTHER INFORMATION: N = any nucleotide
US-09-829-381D-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.05e-29
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ORGANISM: Alyssum spp
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                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION NUMBER: 99042/SEE.36525/US/A
TELECHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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; Sequence 48, Application US/08377687
; Patent No. 5238525
; APPLICANT: BROEKART, WILLEM F.
APPLICANT: CAMMUE, BRUND P.A.
APPLICANT: CAMMUE, BRUND P.A.
APPLICANT: TERRA, FRAM B.
APPLICANT: TERRA, FRAM B.
APPLICANT: TERRA, FRAM B.
TITLE OF INVENTION: BIOCIDAL PROTEINS NUMBER OF SEQUENCES: 59
COMRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN DARDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USP
                                                            TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
SOFTWARE: PatentIn version 3.1
                                                                                                                          ; OTHER INFORMATION: Synthetic US-09-829-381D-16
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
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Best Local Similarity:
Query Match:
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                    SEQ ID NO 16
LENGTH: 285
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APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contro
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AAGAACCAATGCATCAACCTCCAGAAGGCACGGCATGGATCTTGCAACTACGTCTTCCCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AAGTIGIGGAGAGGCCATCAGGGACTIGGICAGGAGTCIGCGGAAACAACAACGCAIGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
    NUMBER OF SEQUENCES: 20
CARRESPONDRICE ADDRESS:
ADDRESSEB: Clarles B. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
                                                                                                                                                       COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
MUDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTONEY/AGERT INFORMATION:
NAME: COCHEN, Charles E.
REGISTRATION NUMBER: 34.565
REGISTRATION NUMBER: 34.565
REGISTRATION NUMBER: 34.565
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRA: (314) 537-6047
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LEMETH: 285 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285
45
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AlaHisLysCysIleCysTyrPheProCys 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09829381D Patent No. 6653280 GENERAL INFORMATION:
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96.00%
90.00%
92.79%
                                              ADDRESSEE: Charl
STREET: 700 Chest
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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Best Local Similarity:
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Pred. No.:
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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
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MEDIUM TYPE: FOLDSPY disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
OPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-No. 618/904-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION AUMBER: US/08/02,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INPORMATION:
NAME: KOKULIS: PAUL N.
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
                                                                                                                                                                                          414
2 2 3 3 0 0 0 0 0
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Matches:
Conservative:
Mismatches:
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TERRAS, FRANKY R.G.
VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                 US-10-681-972-2 (1-50) x US-08-777-192-48 (1-414)
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                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BROEKAERT, WILLEM F. CAMMUE, BRUNO P.A. OSBORN, RUPERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-971-982-48; Sequence 48, Application US/08971982; Patent No. 6187904; Patent No. 6187904;
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TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
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96.00%
90.00%
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ZIP: 20005
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                          ; FEATURE;
; NAME/KEY:
; LOCATION:
US-08-777-192-48
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET UNBER: 16,773
REFERENCE/DOCKET UNBER: 16,773
REFERENCE/DOCKET UNBER: 16,773
RELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
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Mismatches:
Indels:
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                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 AlaHisLyBCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMUEL, BRUNO P.A.
APPLICANT: OSBORN, RUBERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 48, Application US/08777192
Patent No. 5824869
GENERAL INFORMATION:
                                                                                                                                                                                          1.1e-27
283.00
96.00%
90.00%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
    TYPE: nucleic acid STRANDEDNESS: both
                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                   ; NAME/KEY: CDS
; LOCATION: 16..255
US-08-377-687-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-777-192-48
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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                      NAME/KEY: CDS

LOCATION: 16..255

SEQUENCE DESCRIPTION: SEQ ID NO: 48:

US-08-971-982-48
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
                                                                                                      1.1e-27
283.00
96.00%
90.00%
                                                                                              Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-681-972-2 (1-50) x US-08-971-982-48 (1-414)

Search completed: May 18, 2004, 21:56:21 Job time : 64 secs

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Sequence 48, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 58, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 2046, Ap
Sequence 21, Appl
Sequence 21, Appl
Sequence 31, Appl
Sequence 31, Appli
Sequence 31, Appli
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 37, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
                                                       Sequence 12, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appl
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21, Appl
3, Appli
17, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, App]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Sequence Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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TITLE OF INVENTION: Antifungal Polypeptide and Methods
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                             US-09-732-561-13

US-09-829-381A-17

US-09-829-381A-17

US-09-829-381A-5

US-10-811-972-5

US-10-938-842A-2046

US-09-938-842A-2046

US-09-938-842A-2046

US-09-938-842A-2046

US-09-938-842A-2046

US-09-938-842A-2046

US-09-938-842A-204

US-09-732-561-15

US-09-732-561-21

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US-09-732-84-34

US-09-732-84-34

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US-09-732-84-34

US-09-732-84-34

US-09-738-8449A-15

US-09-738-8449A-15

US-10-178-449A-15

US-10-178-449A-15

US-10-178-449A-19

US-10-178-449A-19

US-10-178-449A-19

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US-10-178-449A-19

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US-10-178-449A-19

US-10-178-449A-19

US-10-178-449A-19
US-09-829-381A-14
3 US-10-681-972-14
3 US-09-829-381A-12
3 US-10-681-972-12
3 US-10-681-972-12
3 US-10-681-972-16
3 US-10-681-972-16
3 US-10-681-972-16
3 US-10-81-972-16
3 US-10-81-972-16
4 US-10-188-361A-48
4 US-10-006-252A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
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ADDRESSEE: Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
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STATE: Missouri
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        US-09-829-381A-14
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                Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-DE=Published Applications NA -OFMT=fasEap -SUFFIX=p2n.Tnpb -MINMATCH=0.1
-LOOPCLI=0 -LOOPEXT=0 -UNITS=bits -START=1 -BND=-1 -MARKXEAblosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=USI0681972 @CGN 1 1 164 @rumat 17052004 151741 4466
-NCPU-6 -ICPU-6 -ICPU-3 -NO MAAP -LARGEQUERT NBG SCORE=0 -WAIT -DSPBLOCR=100
-LONGLOG -DEV TIREOUT=120 -WARN TIMEOUT=30 -THREADS=1 -SCAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                       May 18, 2004, 21:15:19 ; Search time 289 Seconds (without alignments) 785.130 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                305
1 RLCERPSGTWSGVCGNNNAC......BHGSCNYVFPAHKCICYFPC 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
15: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                        - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2947324 segs, 2269024515 residues
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Searched:

0.5

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

**BLOSUM62** 

Scoring table:

US-10-681-972-2

Perfect score:

Sequence:

OM protein

Run on:

SUMMARIES

Length DB

Query Match

Score

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40
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                             1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                            21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu, Yonie. S.
Wu, Yonie. Cindy A.
Rosenberger. Cindy A.
ROSENDERGER. Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
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                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PASTENTIN Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
                                                                                                                                                                                                       US-10-681-972-2 (1-50) x US-10-681-972-14 (1-270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 Gercacaargrarirgraacireeeargr 258
                                                                                                                                                                                                                                                                                                                                                                                                          41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRILICATION NOWAND PERIOD FILING DATE: 09-Apr-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 09/103,489
APPLICATION NUMBER: 09/103,489
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REGISTRATION NUMBER: 34,565
                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                             305.00
100.00%
100.00%
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STATE: Missouri
COUNTRY: USA
                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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                                      Alignment Scores:
Pred. No.:
  US-10-681-972-14
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REPERBURE: 38-21 (10700) C.
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT PAPLICATION NUMBER: US/99/829,381D
PRIOR PLING DATE: 2001-04-09
PRIOR PLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
LENGTH: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-066-24

ATTORNEY/ABGNI INFORMATION:

NAME: Cohen, Charles E.

REGISTRATION NUMBER: 34-565

REFERENCS/DOCKET NUMBER: 38-21 (10700) A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6224

TELEPHONE: (314) 537-6047

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 270 base pairs

TYPE: nucleic acid

STANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.27e-33
305.00
100.00%
100.00%
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OTHER INFORMATION: Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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US-10-681-972-14
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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
CORRESPONDENCE: Charles E. Cohen, Monsanto Company, BB4F
STRET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ArgieucysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
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                                                     APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                         COMPUTER FEATABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: CC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: CURKNOWN>
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APPLICATION DATA:

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNEY/AGENT INFORMATION:

RAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565

REGISTRATION NUMBER: 38-21 (10700)A

TELEPRANCATION INFORMATION:

TELEPRANCE, (314) 537-6047

INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID
Sequence 9, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 9, Application US/10681972; Publication No. US20040064850Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.17e-32
296.00
98.00%
96.00%
97.05%
                                                                                                                                                                   NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                              ZIP: 63198
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Best Local Similarity:
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REPERENCE: 38-21 (10700) C.
CURRENT APPLICATION NUMBER: US/10/681, 972
CURRENT PILING DATE: 2003-10-09
PRIOR FILING DATE: 2001-04-09
PRIOR PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SSOTHWARE: Patentin version 3:1
SSOTHWARE: Patentin version 3:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AGGITGIGGGAGAGAGCAAGIGGGAGTGGGAGGTTTGIGGGAACAACAATGCATGC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                           21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
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                                                                                                                                                                        1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
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Matches:
Conservative:
Mismatches:
Indels:
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       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                    US-10-681-972-2 (1-50) x US-09-829-381A-12 (1-286)
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                                                                                                                                                                                                                                                                                                                                        41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                     41 AlaHisLysCyslleCysTyrPheProCys 50
                                                                               Indels:
                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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305.00
100.00%
100.00%
       1.37e-33
305.00
100.00%
100.00%
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Best Local Similarity:
                                             Percent Similarity:
Best Local Similarity:
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US-09-829-381A-9
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                                                                                   Query Match:
           Pred. No.:
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Sequence 16, Application US/10681972

Sequence 16, Application Wolfold850A1

Publication No. US20040064850A1

SEQUENCE II. Application No. US20040064850A1

SEQUENCE II. Liang, Jihong

APPLICANT: Riang, Jihong

APPLICANT: Rosenberger, Cindy A.

APPLICANT: Rosenberger, Cindy A.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Plant Pathogenic Fungi

TITLE OF INVENTION: Plant Pathogenic Fungi

TITLE OF INVENTION: Plant Pathogenic Fungi

TITLE OF INVENTION: Plant Pathogenic Fungi

TITLE OF INVENTION: Plant Pathogenic Fungi

FILE REFERENCE: 38-21 (10700) C,

CURRENT APPLICATION NUMBER: US/09/829,381D

PRIOR FILING DATE: 2001-04-09

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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245
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FILING DATE: 09-Apr-2001
CLASSIFICATION: ¢Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECHMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEPHONE: (314) 537-6224
TELEPHONE: (314) 537-6047
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-829-381A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-681-972-2 (1-50) x US-09-829-381A-16 (1-285)
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                                                                                                                                                                                                                                                                                                                    LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.66e-30
283.00
96.00%
90.00%
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OTHER INFORMATION: Synthetic
US-10-681-972-16
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Best Local Similarity:
Query Match:
DB:
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LENGTH: 285
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         APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: W. Younie S.
APPLICANT:
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contro TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
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CORRESPONDENCE ADDRESS:
ADDRESSEB: Charles E. Cohen, Monsanto Company, BB4F
STREST: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/09829381A
Sequence 16, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Attifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
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COMPUTER: IBM PC compatible
SOBRATURO SYSTEM: PC-DOS/MS-DOS
SOPFATURE: Patentin Release #1.0, Version #1.30
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/09/829,381A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: N = any nucleotide US-10-681-972-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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98.00%
96.00%
97.05%
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ZIP: 63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Alyssum spp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-829-381A-16
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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
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Mismatches:
Indels:
           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                            US-10-681-972-2 (1-50) x US-09-759-584-48 (1-414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANI: Fant, Franky
APPLICANI: Fant, Franky
APPLICANI: Borremans, Frans
APPLICANT: Borremans, Frans
APPLICANT: Bijtsma, Lolke
APPLICANT: Sijtsma, Lolke
APPLICANT: Willem Robbert
APPLICANT: Brijk, Wouter
APPLICANT: Broekert, Wilhelmus
APPLICANT: Broekert, Wilhelmus
APPLICANT: Broekert, Wilhelmus
APPLICANT: Broekert, Wilhelmus
APPLICANT: Wan Gelder, Wilhelmus
APPLICANT: Wan Gelder, Wilhelmus
APPLICANT: Wan Gelder, Wilhelmus
APPLICANT: Wan Gelder, Wilhelmus
APPLICANT: Wan Gelder, Wilhelmus
APPLICANT: Wan Gelder, Wilhelmus
APPLICANT: Wan Gelder, Wilhelmus
APPLICANT: Wan Gelder, Wilhelmus
APPLICANT: Wan Gelder, Wilhelmus
APPLICANT: Wan Gelder, Wilhelmus
APPLICANT: Wan Gelder, Wilhelmus
APPLICANT: WINMER: US/09/77,948
PRIOR APPLICANT: WINMER: US/09/77,948
PRIOR FILING DATE: 1996-03-13
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-03-28
PRIOR FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSEQ for Windows Version 4.0
SEGUTONO 4.0
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Matches:
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283.00
96.00$
90.00$
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           ,69e-30
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                               283.00
96.00%
90.00%
92.79%
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                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-388-361A-45
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Alignment Scores:
Pred. No.:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20005
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99042/SEE.36525/US/A
                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                    US-10-681-972-2 (1-50) x US-10-681-972-16 (1-285)
                                                                                                                                                                                                                                                                                                                                                                        241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
                                                                                                                                                                                                                                                                                                                                             41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 48, Application US/09759584
Patent No. US20010014732A1
GENERAL INFORMATION:
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TENRAS, FRANKY R.G.
APPLICANT: TENRAS, FRANKY R.G.
APPLICANT: VANDERLEXDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES. 59
CORRESPONDENCE ADDRESS:
                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SI
TELEPHONE: 202-861-3000
TELEFAX: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 414 base pairs
TYPR: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                     1.66e-30
283.00
96.00%
90.00%
                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
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; LOCATION:
US-09-759-584-48
       Alignment Scores:
Pred. No.:
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
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ROSENDENTION: Antifungal Polypeptide and Methods
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 1980
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
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Indels:
                                                                                                                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-681-972-2 (1-50) x US-09-732-561-13 (1-403)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3e-29
278.00
96.00%
88.00%
91.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN: PDF 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
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    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 AAGTTGTGCGAAAGGCCCAAGTGGACATGGTCAGGAGTTGTGGGAAACAATAACGCATGC 165
166 AAGAATCAGIGCATTAACCTIGAGAAAGCACGACATGGATCTIGCAACTATGTCTTCCCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ArgheuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
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8 3 3 0 0 0 0 0 0
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APPLICANT: Thomma, Bart
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEB: ZENECA AG Products
STREET: 1800 Concord Pike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                         Sequence 19, Application US/10006252A

Sequence 19, Application US/10006252A

PUBLICANT: De Samblanx, Genoveva

APPLICANT: Broekaert, Willem

APPLICANT: Broekaert, Willem

APPLICANT: Rees, Sarah

TITLE OF INVENTION: Antifungal Proteins

FILE REFERENCE: SIN-034DV

CURRENT FILING DATE: 2001-12-04

PRIOR PELLON NUMBER: 09/077,951

PRIOR FILING DATE: 1998-06-10

PRIOR PELLON NUMBER: GB 9525474.4

PRIOR FILING DATE: 1995-12-13

PRIOR APPLICATION NUMBER: GF 9526703065

PRIOR FILING DATE: 1996-12-12

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PALENTIN VEY: 2.0

SECTION 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                       226 gerekekadrarenderaerreerad 255
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                                                                     41 AlaHisLysCysIleCysTyrPheProCys
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Patent No. US20020035738A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283.00
96.00%
90.00%
92.79%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA; ORGANISM: Raphanus sativus
US-10-006-252A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                          RESULT 11
US-10-006-252A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-732-561-13
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Pred. No.:

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KORULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
BAPLICATION NUMBER: US/09/759,584
                                                                                                                                                                                                Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                            Mismatches:
                                                                                                                                                                                                                                                                                                                                        US-10-681-972-2 (1-50) x US-10-681-972-17 (1-285)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 58, Application US/09759584
; Sequence 58, Application US/09759584
; Patent No. US2010014732A1
; APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: CARMUE, BRUNO P.A.
; APPLICANT: PERES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDBN, JOZEF
TITLE OF INVENTION: BLOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSE:
ADDRESSEE: CUSHMAN DARRY
                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 285
                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                              3.02e-29
274.00
94.00%
86.00%
89.84%
                                                                                                  FEATURE:
OTHER INFORMATION: Synthetic
US-10-681-972-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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Sequence 17, Application US/10681972

Publication No. US20040064850A1

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Plant Pathogenic Fungi

TITLE OF INVENTION: Plant Pathogenic Fungi

FILE REPRENCE: 38-21 (10700) C.

CURRENT APPLICANTION NUMBER: US/10/681,972

CURRENT FILING DATE: 2003-10-09

PRIOR FILING DATE: 2001-04-09

PRIOR FILING DATE: 2001-04-09

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys 20
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                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285
4 4 8 0
0 0
                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELEPHONE: (314) 537-6224
TELEPHONE: (314) 537-6047
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-829-381A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-681-972-2 (1-50) x US-09-829-381A-17 (1-285)
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                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION SURROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.02e-29
274.00
94.00%
86.00%
89.84%
  COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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274.00
94.00%
86.00%
TYPE: nucleic acid
STRANDENNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FRATURE:
NAME/KRY: CDS
LOCATION: 43.282
US-09-759-584-58
                                                                                                   Pred. No.: 3
Score: 2
Percent Similarity: 9
Best Local Similarity: 80
Query Match: 81
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US-10-681-972-2 (1-50) x US-09-759-584-58 (1-288)

288 4 4 8 0 0 0 3 4 4 3 0

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41 AlaHiBLYSCYSILECYSTYPHEPROCYS 50

Search completed: May 18, 2004, 22:55:50 Job time: 290 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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(without alignments) 631.870 Million cell updates/sec US-10-681-972-2 305 1 RLCERPSGTWSGVCGNNNAC......EHGSCNYVFPAHKCICYFPC 50 May 18, 2004, 20:22:48 ; Search time 2363 Seconds OM protein - nucleic search, using frame\_plus\_p2n model Title: Perfect score: Run on:

27513289 segs, 14931090276 residues 0.0 0.5 0.5 Xgapop 10.0 , Xgapext (Ygapop 10.0 , Ygapext (Ygapop 6.0 , Fgapext Delop 6.0 , Delext ... **BLOSUM62** Scoring table: Sequence: Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1h
-MODEL=frame+ p2n.model -DEV=x1h
-Q=/cgn2\_1/USPTO\_spool/US10681972/runat\_17052004\_151740\_4363/app\_query.fasta\_1.199
-Q=/cgn2\_1/USPTO\_spool/US10681972/runat\_17052004\_151740\_4363/app\_query.fasta\_1.199
-DB=EST -Q=VT=fastap -SUFFIX=p2n.ret -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNINS=bits -START=1 -END=1 - MARRIX=blosum62 -TRANS=buman40.cdi -LIST=45
-UOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL
-USER=VS10681972\_@CGN 1 1\_2135\_@runat\_17052004\_151740\_4363 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NGS\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DBV\_TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPPOF=10 -XGAPEXT=0.5 -FGAPOP=6

EST: \*

Database :

ges vrt:\* em\_esthum:
em\_estin:
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gb\_estl:
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gb\_est2:
gb\_est2:
gb\_est2:
gb\_est4:
em\_estfun: em\_gss\_pro:\* em\_gss\_rod:\* em\_gss\_hum:\* em\_gss\_inv:\* em gss pln:\* em gss mam:\* em\_gas\_mus:\* em\_estom:\* em estba:\* em\_gss\_ 16: 17: 18: 

em\_gss\_rcc: em\_gss\_vrl:\* gb\_gssl:\*

gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1111111	833779 BN45.0	834090 BN45.0	832625 BN40.0	8	833944 BN45.0	826491 BN25.0	31111 BN40.0	33977 BN45.0	33983 BN45.0	27413 BN25.0	31294 BN40.0	31479 BN40.0	1068 BN45.0	592 BN40.0	611 BN45.0	2071 BN40.0	1008 BN45.0	1994 BN45.0	L680 BN40.0	3332 BN25.0	1014 BN40.0	3392 BOGWE	1972 BN40.0	157 32717 Lam	1454 DS01	118 AV81611	AV7879	2294 BN40.	1852 BN45.0	3613 BN40.	3047 BN40.	1226 BN40.	HAYD BINAD.	1092 BN45.	2924 BM45	833627 RN45 00	33661 BN45	828840 BN40 04	830628 BN40 04	TO OVING OCYOCO	TOTAL STATE	29 BOMSG	337517 BN45.05	33048 BN40.06	33938 BN45.04
SUMMARIES 1 DB ID	1 1	14 CD83377	14 CD83409	14 CD83262	14 CD8341	14 CD83394	14 CD82649	14 CD83111	14 CD83397	14 CD83398	14 CD82741	14 CD83129	14 CD83147	14 CD83406	14 CD83259	14 CD83461	14 CD83207	14 CD83400	14 CD83499	14 CD83168	14 CD82833	14 CD83101	28 BH45839	14 CD83197	9 AA713157	12 BG3214	9 AV81611	AV787956	14 CD83229	14 CD8348	14 CD83361	14 CD83304	14 CD83122	14 CD83499	14 (1083378	74 (002200)	14 (1833.62	14 CD83366	14 CD82884	14 (1083062	2000000	14 CD82942	28 BZ51772	14 CD83751	14 CD83304	14 CD83393
% Query Score Match Length	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	33 92.8 40	33 92.8 40	33 92.8 41	33 92.8 41	33 92.8 42	33 92.8 42	33 92.8 42	33 92.8 42	33 92.8 42	33 92.8 42	33 92.8 43	33 92.8 43	33 92.8 44	33 92.8 44	33 92.8 45	33 92.8 45	33 92.8 45	83 92.8 45	83 92.8 47	83 92.8 48	83 92.8 55	83 92.8 80	79 91.5 42	78 91.1 31	78 91.1 39	78 91.1 42	278 91.1 422	77 90.8 40	77 90.8 42	77 90.8 42	77 90.8 44	77 90.8 45	77 90.8 47	77 90.8 47	77 0 00 0	77 90 8 48	77 90.8 52	47 8 00 77	40 8 00 77	0.00	40 00.00 04	77 90.8 76	74 89.8 42	74 89.8 42	73 89.5 52
Result No.		7	7	e	4	S.	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	N.	c 26	c 27	28	29	30	31	32	200	ህ Co	3 6	2 6	. 60	9.6	9 4		Į.	24.	4.3	44	45

EST 10-JUL-2003 Bukaryota; Vinidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. CD833779 408 bp mRNA linear EST 10-JUL-2003 BN45.001115F010914 BN45 Brassica napus CDNA clone BN45001115, mRNA CD833779.1 GI:32515719 EST. Brassica napus (rape) Brassica napus sequence. CD833779 DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE RESULT 1 CD833779

ALIGNMENTS

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Pred. No.:

Score:

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ORIGIN

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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CD832625 GR3261227 BN40 Brassica napus cDNA clone BN40064A14, mRNA sequence.
CD832625,1 GI:32514565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Tosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases I to 418)
Genoplante.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoplante, a major partnership french program in plant genomics (Mopublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                              1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
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Matches:
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                                                                                             93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Genoplante, a major partnership french program in plant genomics
Uppublished (2003)
Contact: Genoplante
Genoplante
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                Genoplante.
Genoplante, a major partnership french program in plant
Uppublished (2003)
Contact: Genoplante
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Gaps:
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CD834090.1 GI:32516030
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Brassica napus
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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CD826491 421 bp mRNA linear EST 10-JUL-2003
BN25.064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, mRNA
sequence.
                                      CD833944 110-JUL-2003 RRNA linear EST 10-JUL-2003 EN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, RRNA
                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Genoplante, a major partnership french program in plant genomics
Upublished (2003)
Contact: Genoplante
Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).
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                                                                                                                                                       203 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGGATCTTGCAACTATGTTCCCA 262
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Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
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                                                       1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93, rue Henri Rochefort 91025 BVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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                 US-10-681-972-2 (1-50) x CD832625 (1-418)
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US-10-681-972-2 (1-50) x CD833977 (1-421)
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Brassica napus (rape)
Brassica napus
Brassica, viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Spermatophyta, magnoliophyta, eudicotyledons, core eudicots,
I spermatophyta, II; Brassicales, Brassicaceae, Brassica.
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                                                                                                              Tue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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Mismatches:
Indels:
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CD831111.1 GI:32513051
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Best Local Similarity:
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CD833977 421 bp mRNA linear EST 10-JUL-2003 BN45.040D05F011019 BN45 Brassica napus cDNA clone BN45040D05, mRNA sequence.
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Brassica napus
Brassica napus
Brassica napus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
1 (bass 1 to 421)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
                                                                                                                                                                                                                      141 AAGTIGIGGGAGAGGCCAAGIGGGACAIGGICAGGAGICIGIGGAAACAAIAACGCAIGC 200
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Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                        1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
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Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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438 bp mRNA linear EST 10-JUL-2003 BN40.058N13F011019 BN40 Brassica napus CDNA clone BN40058N13, mRNA Bequence. CD831294
CD831294
CD831294.1 GI:32513234
CD827413 426 bp mRNA linear EST 10-JUL-2003
BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
1 (bases 1 to 438)
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                                                                                                                                                                                                                                                                                                                                             93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
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Unpublished (2003)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                            CD827413
CD827413.1 GI:32509353
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Brassica napus
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Genoplante
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CD831294
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BN45.040D11F011019 BN45 Brassica napus CDNA clone BN45040D11, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica napus
Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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                                                                                                    93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Contact: Genoplante
                                                          141 AAGTTGTGCGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC
                       1 ArgieuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
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45
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Matches:
Conservative:
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Indels:
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96.00%
90.00%
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FEATURES

Percent Similarity: Best Local Similarity: Query Match:

41

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RESULT 10 CD827413

Alignment Scores:

ORIGIN

No.:

Score:

Genoplante.

REFERENCE AUTHORS TITLE JOURNAL COMMENT

sequence. CD833983

DEFINITION

RESULT 9 CD833983

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Genoplante

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CD834068 446 bp mRNA linear EST 10-JUL-2003 BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA sequence.
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Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Fins sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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Matches:
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Mismatches:
Indels:
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Brassica napus (rape)
Brassica napus
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CD834068
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 438)
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Contact: Genoplante
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Location/Qualifiers
                             93. The Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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Gaps:
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/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40059J3"
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cultivar="Jet neuf"
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/clone="RNA4058N13"
/tissue type="seed"
/clone_lib="BN40"
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-681-972-2 (1-50) x CD831294 (1-438)
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CD831479.1 GI:32513419
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96.00%
90.00%
92.79%
   Contact: Genoplante
Genoplante
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CD831479
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                                                                                                                                                                                  CD832592
BN40.063015F011228 BN40 Brassica napus CDNA clone BN40063015, mRNA
                                                                                                                                                                                                                                                                                       Brassica napus
Wharyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II, Brassicales, Brassicaceae; Brassica.
1 (bases 1 to 447)
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                                                        216 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAAGTGTCTTCCCA 275
40
                                        ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                             93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Flas sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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/mol_type="mRNA"
/cultivar="Jet neuf"
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/tissue_type="seed"
/clone_lib="BN40"
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Genoplante
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Brassica napus Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 450)
                                                                                                                                                                                    Genoplante. Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                             93. The Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Fix sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Mismatches:
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CD834611.1 GI:32516551
                                                Brassica napus (rape)
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